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Search completed: May
Job time: 7263.7 secs
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
        AUTHORS
TITLE
JOURNAL
                                                                 REFERENCE
AUTHORS
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                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                         /Glone lib="Plasmodium yoelli 17% axenic hepatic stages"
/note="Vector: pCR4.0TOPO; 10 million plasmodium yoelii
17% sporozoites were isolated from salivary glands of
infected Anospheles stephensi mosquitoes and purified over
a DB52 cellulose column. The sporozoites were cultured for
24h at 37c in the presence of $$ CO2 and 10% FBS as
described in Transformation of sporozoites into early
excerythrocytic malaria parasites does not require host
cells (U Exp Med. (2003)197 (8):1045-50; mRNA was
extracted using the Invitrogen microFAST TRACK kit and
used for cDNA construction via the BDBiosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
kit."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AATAAGATCACTCTGTACATCCACATACAGTACGATAACCGNCTCTCTNTTTTATAGGTC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 GCCTGACATTTATATTCCCCCAGAACATCAGGTTAANGGCGTTTTTGATGTCATTTTCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 TTTATCTGACAGCAGAGTGCACTGGCCAGGGGGATCACCATCGTCGCCCCGGCGTGTC
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$4000791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 271.8; DB 14; Length 1037; 91.9%; Pred. No. 1.4e-36; live 0; Mismatches 24; Indels 2;
New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanopol@med.nyu.edu
No Blast Hite ().
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                                                                                                                                                        /organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17%"
                                                                                                                                                                                                                                      db_xref="taxon:73239"
dev_stage="axenic hepatic stages"
lab_host="E. coli TOP10"
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                                                                                                                                                                                                                     sub_species="yoelii"
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Homo sapiens
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                                                                                                                                       . .1037
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Matches 294; Conserv
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DEFINITION
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Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q,
Published Only in DataBase (1997)
2 (bases 1 to 724)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (B-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.6%; Score 264.4; DB 29;
ilarity 98.6%; Pred. No. 2.8e-35;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                  1. .724
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="21q"
/clone="64E11X4"
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//lone lib="Plasmodium yoelli 17X axenic hepatic stages"
//lone lib="Plasmodium yoelli 17X axenic hepatic stages"
//note="Vector: pCR4.0T0P0; 10 million Plasmodium yoelii
//note="Vector: pCR4.0T0P0; 10 million Plasmodium yoelii
//note="Vector: pCR4.0T0P0; 10 million Plasmodium yoelii
//note="Vector stages"
//note="Vecto
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1 (bases 1 to 1037)
Wang,Q., Okubo,E., Kaiser,K., Pashrel,E., Kappe,S., Brown,S.,
Nussenzweig,V. and Bhanot,P.
Expressed sequence tags from Plasmodium yoelli hepatic stages in axenic culture
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                                                                     'organism="Plasmodium yoelii yoelii"
                                                                                                                                                             sub_species="yoelli"
(db_xref="taxon:73239"
dev_stage="axenic hepatic stages"
(1ab_host="E, coli TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 273.2; DB 14
llarity 90.0%; Pred. No. 7.7e-37;
Conservative 0; Mismatches 31.
                                                                                               /mol_type="mRNA"
/strain="17X"
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Plasmodium yoelii yoelii
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Contact: Bhanot P
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tes 278; Conserv
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Best Local Si
Matches 278;
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                                                                                                                                                                                                                                                                                       /organism="Ipomoea nil"
/organism="Ipomoea nil"
/mol type="mRNA"
/cultivar="Towor.yoc-kokei standard"
/db_xref="taxon:35883"
/db_xref="taxon:35883"
/db_xref="taxon:35883"
/db_xref="taxon:35883"
/db_xref="taxon:35883"
/db_xref="taxon:35883"
/clone="mixture of flower and flower bud"
/clone="lib="Ipomoea nil mixture of flower and flower bud"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 TGGC-TTTTTGATGCCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGGATAACGG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666 AGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCCCGATATGCA 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AGACCGGCACACTGGCCATATCGGTGGTCATGATGCGCCAGCTTTCATCCCCGGATATGCA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               786 TCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGAT 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 TCACCATCCGTCGCCCGGGCGTCTCAATAATATCACTCTGTACATCCACAAAACAGACGAT 322
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550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanopol@med.nyu.edu
similar to NR[GI-23483806 hypothetical protein [Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 TGGCGTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGG
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Plasmodium yoelii yoelii
Bukaryota; Alveelata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1068)
Wang, C., Okubo,B., Kaiser,K., Pashrel,E., Kappe,S., Brown,S.,
Wussenzweig,V. and Bhanot,P.
Expressed sequence tags from Plasmodium yoelii hepatic stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%; Score 301.4; DB 12; Length 337; ilarity 99.4%; Pred. No. 1.8e-41; Conservative 0; Mismatches 1; Indels 1;
Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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Department of Pathology
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CF469981/c
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BJ555980 Ipomoea nil mixture of flower and flower bud Ipomoea nil BJ555980 BJ555980 GDNA clone jml8n08 5', mRNA sequence.
BJ555980 GI:27237800 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The CDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 CATTIGGAAGGCIGICGGICGACIAAGIIGGCAGCAICACCCGAAGAACAIIIGGAAGGC 127
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1 (bases 1 to 337)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S. ESTs of Japanese morning glory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3616 TAATACGGCATTGAGGACAATAGCGAGTAGGCTGGATACGACGATTCCGTTTGAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 TAATACGCATTCAGGACAATAGCGAGTAGGTTGGATACGACGATTCCGTTTCAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3676 CATTIGGAAGGCTGTCGGTCGACTAAGTIGGCAGCATCACCCGAAGAACATTIGGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 rerederesacracaegreacraaaegecareraagraerrearrearaereacresarar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 TGTTCTTGATGCAGATGTTTTCAGGACTATGACACTAGCGTATATGAATAGGTAAAATGT
                                                                                   Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans C
cloning project: Contact jerome_reboul@dfci.harvard.edu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 384;
                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 325.4; DB 12; 98.2%; Pred. No. 1.4e-45; iive 0; Mismatches 6;
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        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         male"
                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:6239"
/sex="Hermaphrodite and male
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tpomoea nil (Japanese morning glory)
           Boston, MA 02115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
                                                                                                                                                                                                       philippe_vaglio@dfci.harvard.edu_
POLYA=No.
                                                                                                                                                                                                                                                                   Location/Qualifiers
44 Binney Street,
Tel: 617 632 5180
Fax: 617 632 2425
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Nat. Genet. 27 (3), 332-336 (2001)
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OSTF043E11_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
                                                                                                                                                                                           /db_xref="taxon:6219"
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/fissue_type="whole animal"
/fissue_type="whole animal"
/dow_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNAs were cloned into pPC86"
philippe_vaglio@dfci.harvard.edu
POLYA=No.
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Dana Farber Cancer Institute
                                                           Location/Qualifiers
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                                                                                                                                              /mol_type="mRNA"
/strain="N2"
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DEFINITION ACCESSION VERSION ORGANISM

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Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F., Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans

Nat. Genet. 27 (3), 332-336 (2001)
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
/clone_lib="AD-wrmcDNA" library was generated with poly(A) + /note="The AD-wrmcDNA library was generated with poly(A) + AD-with stages from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                  487;
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Pred. No. 2.3e-49;
0; Mismatches 11;
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Marc Vidal Laboratory
Dana Farber Cancer Institute
14 Binney Street, Boston, MA 02115,
141: 617 632 5180
Fax: 617 632 2425
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Sequence tag of Gateway entry clones. The primers used were
Sequence tag of Gateway entry clones. The primers used were
closigned on the predicted protein encoding ORF. C. elegans ORPeome
cloning project : Control david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
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Enkaditoidaa; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 487)
Reboul.J., Vaglio, P., Rual.J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Lil.S., Jacoctot, L., Bertin, M., Janky, R., Moore, T.,
Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.
Endress, G.A., Jenna, S., Chevet, S., Papasotiropoulos, V.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M. Chance, M.R., Lee, H.,
C. elegans ORFeome version 1.1: experimental verification of the
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OSTRI51B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB395230
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Tel: 617 632 5180
Fax: 617 632 5739
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/tissue_type="whole animal"
/dev_stage="mixed stage"
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Dana Farber Cancer Institute
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Contact: Vidal M
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/strain="N2"
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AUTHORS
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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Harley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeene version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB395230 487 bp mRNA linear EST 15-MAY-2003
OSTAT51B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
                                                                                                                                            GATITICCGCTITCCAGCGTICGGCACGCAGACGACGGCCTICATICTGCATGGTTGTGC 1020
                                                                                                                                                                                                                                              TTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTC 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gareway entry clones. The primers used were
Sequence tag of Gareway entry clones. The primers used Nere
Gesigned on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
189 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGT 430
                                                                                            371
                                                                                                                                                                                             370 GATTTTCCGCTTTCCAGCGTTCGGCACGCACGACGACGGCTTCATTCTGCATGCTTGTGC 311
                                                                                                                                                                                                                                                                                            310 TTACCAGACCGGAGATATTGACATC--ATATGCCTTGAGCAACTGATAG-TGTCGCTGTC 254
                                                                                                                                                                                                                                                                                                                                            1081 AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTA 1137
                                                                                                                                                                                                                                                                                                                                                                      253 AACTGTCACTGTAATACGCTTCCTTAGCACACCTCTTTTTGACATACTTCGGGTA 197
                                                TCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCT
                                                                               429 TCTCGTCAGC-AAAGAGCGTTCATTTCAATAAACCGGGGGACCTCAGCCATCCCTTCCT
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
THI: 617 632 5139
Fax: 617 632 5739
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/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 357; DB 14;
Pred. No. 5.2e-51;
0; Mismatches 25;
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/sex="Hermaphrodite and male
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/strain="N2"
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El (Dases I to 722)

Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNA, chromosome 21q

Dublished Only in DataBase (1997)

E (Dases I to 722)

S Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.

Direct Submission

I. Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9722, Fex:0427-78-9561)
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                                                     TCACCATCCGTCGCCCGGGCGTGTCATAATATCACTCTGTACATCACAAAAAAGAGGAT
                                                                                                                                                    323 AACGGCTCTC-TTTATAGGTGTAAACCTTAAACTGCATTTCACCAACCCCTGTTCTCG
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                                                                                                                                                                                                                         TCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCC-TTCCTGATT
                                                                                                                                                                                                                                                             382 TCAGCAAAAGAGCCGTTCATTTCAATAAAACGGGCGACCTCAGCCATCCCTTTCCTGATT
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                         TCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGAT
                                                                                                                        AACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens genomic DNA, 21q region, clone: 64EllX4, genomic AG000763
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Pred. No. 3.8e-58;
0; Mismatches 31; Indels 11:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="64E11X4"
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92.2%;
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AUTHORS
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
ToNA Library Preparation: Michael Jr. Brownstein (NHGRI) with help
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.lln.gov
Plate: NDAM391 row: e column: 05
High quality sequence start: 68
High quality sequence start: 68
High quality sequence stop: 256.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 52.2)
III (bases to 52.2)
INH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pre-eclamptic placenta"
/lab.host="NH10B TonA"
/lab.host="NH10B TonA"
/clone_lib="NH1 MGC 148"
/note="Organ: placenta; Vector: pBluescriptR; Site_l:
all-Khol; Site_2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5.TITITITITITITITITIVN-3; size-selected for average ins
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                                                                                                  AGENCOURT 13894516 NIH MGC 148 Homo sapiens cDNA clone IMAGE:30348484 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 522;
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Pred. No. 4.8e-59;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:30348484"
                 189 rrrrgacaractrcegera 170
                                                                                                                                                                                                           CB997937.1 GI:30292457
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al Similarity 96.2%;
435; Conservative
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Best Local S
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S Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21g
L Published Only in DataBase (1998)
E 2 (bases 1 to 725)
S Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
B 2 Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
L Submitted (07-SEP-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
On Feb 5, 1999 this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1058 AGCAACTGATAGCTGTCGCTGTCAACTGTCAATACGCTGCTTCATAGCACACCTC 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTG 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTTTTATAGGTGT-AACCTTA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         878 AACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCG 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAGGAGCGGTTCATTTCAATAAACCG 367
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                                                                                                                                                 Chordata; Craniata; Vertebrata; Buteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/clone="f32E9X13"
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                                                              GI:3549208
                                                                                                    Homo sapiens (human)
Homo sapiens
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                      survey sequence.
AG013450 AG005773
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

The (bases 1 to 723)

Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

Lublished Only in DataBase (1997)

E 2 (bases 1 to 723)

Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

E 2 (bases 1 to 723)

Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

Direct Submission

Location (all OCT-1997) Masahira Hattori, Kitasato University,

Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,

Tel:0422-78-9732, Fax:0427-78-9561)
                                                 GSS 06-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 TCAGCAAAAGAGCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 CCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGACGAGACGTGCACTGGCCAGGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          786 TCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 TCACCATCGGTCGCCGGGGGTGTCAATAATATCACTCTGTACATCCACAACAGACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIGCAGACIGGCIGIGIAIAAGGGAGCCIGACAITIAIAITAITCCCCAGAACAICAGGIIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 CTGCAGACTGGCTGTGTATAACGGAGCCTGACATTTATATTTCCCCAGAACATCAGGTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666 AGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCCAGCTTTCATCCCCGGTATGCA
                                                 723 bp DNA linear GSS 06-FEI
21g region, clone: 64E11X4, genomic
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llarity 98.1%; Pred. No. 2e-60;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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                                                                          Homo sapiens genomic DNA,
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/clone="64E11X4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="21"
                                                                                                                                                   AG000761.1 GI:2579569
                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                       survey sequence.
                                                                                                                                                                                                                           Homo sapiens
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Matches 416; Conserv
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                                                 AG000761
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AG013450/c
LOCUS
                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
RESULT 4
AG000761/c
LOCUS
                                                                        DEFINITION
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TITLE
JOURNAL
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AUTHORS
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                                                                                                                            ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:30346919"
/tissue_type="Human Placenta"
/lab_hofe="DH10B TonA"
/lab_hofe="UNH MGC 147"
/clone lib="WIH MGC 147"
/clone lib="WIH MGC 147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-khol; Site_2: BamH; Oligo-dT primed using primer
5--TTTTTTTTTTTTTTTTTTY3, siz=selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(WIMH/NH3RI, National Institutes of Health). Note: This is
a NIH_MGC library."
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                    Thistic Signature. Stefan Hansson converse to the produce and advice from Piezo Carnino: Michael J. Brownstein (NHGRI) with help and advice from Piezo Carnino: (RIKEN) constitution from the I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution in formation can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: NDAM387 row: c column: 24
High quality sequence start: 144
High quality sequence start: 144
High quality sequence etce: 251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 TCACCATCCGTCGCCCGGGCGTGTCATAATATCACTGTGTACATCCACGAACAGACGAT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 AACGGCTCTCTTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGCCCCTGTTCTCG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAA 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 AGACCGGCACACTGGCCATATCGGTGGTCATCATGCGTCAGCTTTCATCCCCGGTATGCA 202
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Pred. No. 1e-64;
0; Mismatches 18; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
     cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.5%;
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Best Local Similarity
Matches 493; Conserv
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AGENCOURT 13988518 NIH MGC 147 Homo sapiens CDNA clone
IMAGE:30346919 5', mRNA sequence.
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1 (Dases 1 to 542)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                 599 TATATCCCCGGANCATCNGTTAATGCCGTTTTTTGAAGGNATTTTCGCCGTGGCTGAGAAT
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                                                                                                                                                                                                                                                                                                                                                      643 AGCCACTTCTTCCCCCGATAACGGAGACCGGCACACTGGCCATATCGGTCATCATGCG
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                                                                                                                                                                                                   10.6%; Score 496.6; DB 29; Length 713; 94.2%; Pred. No. 6.7e-75; rive 0; Mismatches 30; Indels 2;
Fax:0427-78-9561)
             Location/Qualifiers
1. 713
Arganism="Homo sapiens"
| Lyge="genomic DNA"
| Lyge="taxon:9606"
| Chromsome="21"
| Arganism="21"
| Clone="64E11X4"
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CD109790.1 GI:30753999
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                                                                                                                                                                                                                                              523; Conservative
Tel:0427-78-9732,
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Matches 52
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I (bases 1 to 713)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published only in DataBase (1997)
2 (bases 1 to 713)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (31-007-1997) Masshira Hattori, Kitasato University,
Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
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Pred. No. 1.3e-78;
0; Mismatches 2; Indels 4;
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EST754514 P15E7 Pla P18G02 Pl

Homo sapi P22B07 Pl

RST39901

TOS0136 T 2283763 P13A3 P1a P8-B8 P1a P7-G5 P1a E87750020 P11-E10 P P13B3 P1a P13B3 P1a P17G11 P1 P21H01 P1 OSTR013H1

OSTR013H1 OSTR015E7 OSTR015E7 P20A07 P1 P13D10 P13D10 P1 P11-D8 P1 HOMO SAPI

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 698)

8 Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q

1 Published Only in DataBase (1998)

8 Attori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission.

1 Direct Submission.

1 Submitted (20-ANG-1998) Masahira Hattori, Kitasato University, Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
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/mol_type="genomic DNA"
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AG000761 Homo sapi
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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GSS 08-FEB-1999

Result 8

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ò	3527	GACACTAGCGTATATGAATAGGTAGATGTTTTTTTTTTT
qq	13403	GACACTAGGGTATATGAATAGGTAGATGTTTTTTTTTTT
ζŏ	3587	ACCTUTITICITATITCTITITATGATTITAATACGGCATTGAGGGCAATAGCGAGTAGG 3646
qq	13343	ACCICTITITICITITITITITITITITITITITITITIT
δλ	3647	CTGGATACGACGATTCCGTTTGAAGAACATTTGGAAGGCTGTCGGTCG
qq	13283	CTGGATACGACGATTCCGTTTGAGAACATTTGGAAGGCTGTCGGTCG
ζ	3707	CAGCATCACCCGAAGAACATTTGGAAGGCTGTCGGTCGACTACAGGTCACTAATACCATC 3766
qu	13223	CAGCATCACCCGAAGAACATTTGGAAGGCTGTGGGTCGACTACAGGTCACTAATACCATC 13164
Qy	3767	TAAGTAGTTGATTCATAGTGACTGGATATGTTGTTTTTACAGTATTATGTAGTGTTT 3826
qu	13163	TAAGTAGTICATICATAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTGTTTT 13104
δλ	3827	TITAIGCAAAAICTAAITIAATAIAITGAIATITATAICATITIACGITICAGG 3886
qu	13103	TITAIGCAAAAICTAAITTAAIAITGAIAITTAIGAAAITTAAGITTTAGAITTCTCGTTCAGC 13044
δ	3887	TITITIGIACAAACTIGICIAGAG 3910
Op	13043	TITITIGIACAAACIIGICICGAG 13020
407		10 20 10 2004 DO 00.06.EA

Search completed: May 10, 2004, 00:06:54 Job time: 1306.43 secs

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APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Wethod and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT APPLICATION DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Version 3.1
ENGTH: 17476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16704 CTCTAGACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATTCAAT 16645
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Pred. No. 1.7e-153;
0; Mismatches 1302; Indels 273; Gaps
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; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-055-001A-24/c
Sequence 24, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
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Best Local Similarity 59.9
Matches 2349; Conservative
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Pred. No. 6.7e-158;
0; Mismatches 6;
APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: BREDSITO, DEMINIC
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 0942.512001
CURRENT APPLICATION NUMBER: US/10/151,690
FRIOR APPLICATION NUMBER: US 10/151,690
FRIOR PELIGNON NUMBER: US 10/151,690
FRIOR PELIGNON NUMBER: US 60/291,973
FRIOR FILING DATE: 2002-05-21
FRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                        ; CTHER INFORMATION: plasmid pDONR212
US-10-151-690-64
                                                                                                                                                                                                                                                                                                                                                       23.5%;
                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial sequence
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Matches 1106; Conservative
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868686	Qy Op	Qy Db	O. do	92y 12b	9 9 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Q _Y Db	oy Op	Qy Db	oy G	Sy q	Sy q	Qy	RESULT US-10-1 ; Seque ; Publi ; GENER ; APPI
Qy 746 GAGACTTTATCTGACAGACGAGACCTGGCCAGGGGATCACCATCGGCCGGGC 805 Db 1659 GAGACTTTATCTGACAGACGACGAGGGGATCACCATCGGCCGGGC 1718 Ob 11619 GTGTCAATAATCACTGTACATCACAAACAGACGATCACCTCTTTTATAG 865 Db 1719 GTGTCAATAATAATCACTCTGTACATCCACAAACAGACGATCACTCTTTTTATAG 1778 Qy 866 GTGTAAAACCTTAAAATCACACACCAGTCCCTGTTCTCGCACAAAAAAACGACCGTTCAT 925 Db 1779 GTGTAAAACCTTAAAACTGCATTTCACCAGTCCCTGTTCTCGCACAAAAAAAA	OY 926 THCAATAAACCGGGCGACCTAGCCATCCTTCCTGATTTTCCGCTTTCGGC 985	QY 986 ACGCAGACGACGGCTTCATTCTGCATGTTGTGCTTACCAGACGGAGATATTGACATC 1045	OY 1046 ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCACTGTCACTGTAATACGCTGCTTC 1105	OY 1106 ATAGCACACCTCTTTTCACATACTTCGGGTA 1137	RESULT 13 US-10-151-690-63 Sequence 63, Application US/10151690 Sequence for US-20030124555A1 GENERAL INFORMATION: APPLICANT: BRASCH, MICHAEL A.	; APPLICANT: CHEC, DAVID ; APPLICANT: LI, XIAO ; APPLICANT: ESPOSITO, DOMINIC ; APPLICANT: BYED, DEVON R.N. ; TITTE OF THE TANDER TO THE TANDER OF THE TANDE		PRIOR FILING DATE: 2002-05-21; PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 NUMBER OF SEC 1D NOS: 64	SOFTWARE: PatentIn version 3.1 SEQ ID NO 63 FINGTH: 4627 TYPE: DAY	CRGANISM: Artificial sequence FEATURE: OTHER OTHER PLASSMICH PROMED PROMED PLASSMICH PROPERTY.	ery M st Lo tches	STACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATTT 85	OY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTC 145 Db 150 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACACATATTCCAGTC 209 OY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGACCGACAGCCTTCCAAA 205 Db 210 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAAA 205

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APPLICANT: BYRD, DEVON R.N.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID PRICE REPEATED.

FILE REPERENCE: 0942.5120001

CURRENT APPLICATION NUMBER: US 10/151,690

PRIOR PILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: US 60/291,973

PRIOR PILING DATE: 2001-05-21

PRIOR PILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PATCHIN VERSION 3.1

SEQ ID NO 62

LENGTH: 4428
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Best Local Similarity 99.5%; Pred. No. 6.6e-158;
Matches 1106; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: plasmid pDONR212
US-10-151-690-62
                                                                                                                                                                                                                                                        TYPE: DNA OKGANISM: Artificial sequence FEATURE:
                     LI, XIAO
ESPOSITO, DOMINIC
    APPLICANT:
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AGGGAGCCTGACATTTATATTCCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT
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RESULT 12
US-10-151-690-62
is Sequence 62, Application US/10151690
is bublication No. US20030124555A1
igeneral information:
i APPLICANT: BRASCH, MICHAEL A.

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Sequence 1, Application US/10151690
Sequence 1, Application US/10151690
Sequence 1, Application VS 0030124555A1
Septimization No. US20030124555A1
Sebricant: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC
FILE REFERENCE: 0942.5120001
CURRENT APPLICATION NUMBER: US/10/151,690
STORENT FILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
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                                                                                                             GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGGATCACCATCGTCGCCCGGGC
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; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61
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Best Local Similarity 99.8
Matches 1110; Conservative
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US-10-151-690-61/c
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Pred. No. 7.3e-159;
0; Mismatches 2;
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NAME/KEY:
MAND/KEY:
MAND/KE
   recombination
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; LOCATION: (3794)..(4537)
; OTHER INFORMATION: puc oriv / RK2 oriT
US-10-357-268-1
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: gene
LOCATION: (2868)..(3677)
OTHER INFORMATION: Kan(r) gene
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LOCATION: (1606)..(2265)
OTHER INFORMATION: Cam(r) gene
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Best Local Similarity 99.8%;
Matches 1110; Conservative
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INFORMATION: attP1
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NAME/KEY: gene
LOCATION: (959)..(1264)
OTHER INFORMATION: ccdB
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DEPLICANT: Kahn, Michael L
APPLICANT: Kahn, Michael L
APPLICANT: Kahn, Michael L
APPLICANT: Mouse, Brent L
APPLICANT: Mortimer. Michael W
APPLICANT: Mortimer. Michael W
TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination
FILE REFERENCE: WSUR-1-20231
CURRENT APPLICATION NUMBER: US/10/357,268
CURRENT FILING DATE: 2003-01-31
PRIOR FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 4892
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702 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA
                                                                                                              686 TCGGTGGTCATCATGCGCCAGCTTTCATCCCCCGATATGCACCACCGGGTAAAGTTCACGG
                                                                                                                                        762 TCGGTGGTCATCTGCGCCCGCCTTTCATCCCCGATATGCACCGGGGTAAAGTTCACGG
                                                                                                                                                                                                      746 GAGACTTTAICTGACAGCAGACGIGCACTGGCCAGGGGGATCACCATCCGTCGCCGGGC
                                                                                                                                                                                                                                                                                             806 GIGTCAATAATATCACTCTGTACATCCACAAACAAGACGATAACGGCTCTCTTTTATAG
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                                                                                                                                                                                                                                  822 GAGACTTTATCTGACAGCAGAGGCACTGGCCCAGGGGGATCACCATCCGTCGCCGGGGC
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; Publication No. US20030219902A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Escherichia coli
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LOCATION: (232)..(275)
OTHER INFORMATION: T1
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NAME/KEY: terminator
LOCATION: (232)..(275)
OTHER INFORMATION: T1
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NAME/KEY: terminator
LOCATION: (73)..(100)
OTHER INFORMATION: T2
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US-10-357-268-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC
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Pred. No. 7e-159;
0; Mismatches 2; Indels 0;
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Best Local Similarity 99.8%;
Matches 1110; Conservative
                                                                                                                                                                                                                                                                                      NAME/KEY: gene
LOCATION: (1303)..(1962)
CTHER INFORMATION: CMR
FEATURE:
NAME/KEY: gene
LOCATION: (2210)..(2442)
CTHER INFORMATION: attP2
                                        LOCATION: (29) .. (260)
OTHER INFORMATION: attP1
FRAUGRE:
NAME/KEY: gene
LOCATION: (556) .. (961)
OTHER INFORMATION: ccdB
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NAME/KEY: gene
LOCATION: (1099)..(1184)
OTHER INFORMATION: ccdA
FEATURE:
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; LOCATION: (3495)..(4134)
; OTHER INFORMATION: ori
US-10-151-690-21
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LOCATION: (2565)..(3374)
OTHER INFORMATION: Kmr
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FEATURE:
NAME/KEY:
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APPLICANT: LI, XIAO
APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REPRENCE: 0942.5120001
CURRENT APPLICATION NUMBER: US/10/151,690
FRIOR APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
NUMBER OF SOFTWARE: PATENTIN OF SECOIL OF SECOIL
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ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: plasmid pDONR201
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US-10-151-690-21
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  ACTCTCAACTTTTATCTTCTTCGTCTTACACATCACTTGTCATATTTTTTACATTACTA 14797
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                                                                                                                               TGTTGTTTATGTAAACAATATATTTATAAATTATTTTTTCACAATTATAAACTATATT 14737
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                                                                             TGATTACAGTTGGGAAGCTGGGTTCGAAATCGATAAGCTTGCGCTGCAGTTATCATCATC 2293
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APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Susan V.
APPLICANT: Weterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: Wing recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23.3
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US-10-055-001A-23/c
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908 GGCTGAGATCAGCCACTTCTCCCCGAIAACGGAGACCGGCACACTGGCCATATCGGTGG 156 TCATCATGCGCCAGCTTTCATCCCCGAIAACGGAGACCGGCCACTCTGGCCATATCGGTGG 16 TCATCATGCGCCAGCTTTCATCCCCCGAIATGCACCACGGGAAAAGTTCACGGGGAGCTT 176 TATCTGACAGCAGCAGCACCTGGCCAGGGGAATCACCACCGGGAAAAGTTCACGGGAGCTT 177 TATCTGACAGCAGCAGCACTGGCCAGGGGAATCACCATCGTCGCCCGGGCGTTCAA 178 TATCTGACAGCAGCAGCACTGGCCAGGGGAATCACCATCGTCGCCCGGGCGTTCAA 179 TATCTGACAGCAGCAGCACTGCCCTGGCAGGGAATCACCATCGTCGCCCGGGCGTTCAA 170 TATCTGACAGCAGCAGCACTGCCCTGGTCATCACCATCGCCCGGGCGTCCAA 171 TATCTGACAGCAGCAGCACTGCCCTGGTCAAAAGACTCTCTTTTATAAGTGTAAA 172 TATCTGACAGCAGTCCCTGTTCTCGTCACCTCGCTCGCCCGGGCGTTCAAA 179 TATCTGACACTCAACTCCACAAAAAAAGACGCTTCATTTATAAGTGTAAA 170 TATCTGACACTCAACTCCAAAAAAAAAAAAAAAAAAAAA	3716 CCGAAGAACATTTGGAAGCCTGTCGGTCCACTACAGGTCACTACACATCTATGTTGTT 3775 17628 CCGAAGAACATTTGGAAGCCTGTCGGTCCACTACAGGTCATATACCATCTAGTAGTT 17687 3776 GATTCATAGTGACTGGATTGTTTTACAGTATTATGTAGTCTTTTTTTT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 13360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Indels 1140;
                                                                                                                                                                terminator region
                                                                                                                                                                         TRATURE:

NAME/KEY: misc feature

LOCATION: (264)...(496)

OTHER INFORMATION: nopaline synthase gene promoter

FEATURE:

NAME/KEY: misc feature

LOCATION: (497)...(1442)

OTHER INFORMATION: npt11 coding region

FEATURE:

NAME/KEY: misc feature

LOCATION: (1443)...(2148)

OTHER INFORMATION: nopaline synthase gene terminator

FEATURE:

selection marker (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

) LOCATION: (2149)..(2706)

) OTHER INFORMATION: a left T-DNA border region

US-10-055-001A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3199.6;
Pred. No. 0;
0; Mismatches
                                    NAME/KEY: misc feature
LOCATION: (13048)..(13279)
OTHER INFORMATION: attP1 recombination site
                                                                                                                                                                gene
                                                                                                                                                              synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.3%;
ilarity 78.5%;
Conservative
                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine
OTHER INFORMATION: ccdB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4460; Conserva
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Qy 4509 TTTTGGTGTATGGGGCCCCAAATGAAGTGCAGACCAACCA	10055 5A1 cer trophe and nrecon US/1 06-111 3.1 -DNA prom prom prom ecomb	; OTHER INFORMATION: pdk2 intron 2 FEATURE: NAME/KEY: misc feature LOCATION: (15062)(15661) OTHER INFORMATION: chloramphenicol resistance gene FEATURE: NAME/KEY: misc feature ; LOCATION: (14387)(14619) ; CHER INFORMATION: attp2 recombination site ; FEATURE: NAME/KEY: misc feature ; LOCATION: (13675)(13980)
QY 3526 TGACACTAGCGTATATGAATAGGTAGATGTTTTTATTTTGTCACACAAAAAGAGGCTCG 3585 Db 16609 TGACACTAGCGTATATGATAGATTTTTTTTTTTTTTTTT	3706 GCAGCATCACCCGAAGAACATTTGGAAGGCTOTCGGTCGACTAACAGTCACTAATACCAT 16789 GCAGCATCACCCCGAAGAACATTTGGAAGGCTOTCGGTCGACTAACAGGTCACTAATACCAT 3766 CTAAGTAGTTGATTCAATATTAACATGAATTTTGATTTTTACGAACTAACAGTCACTAATACCAT 3826 TTTATCGCAAAATCTAATTAATATAATATATTAATAACATATTATGTAGTCTCTTT 16899 TTTATCGCAAAATCTAATTAATATAATATATTAATAACATATTATGTAGTCTCTTTCGTTCG	1750 1750 1756 1762

326 AGAAATAAGAAAAAGGGGGGCGCTCTTTTTTGTGTGACAAAATAAAAACATCTACCT 385 	386 AITCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC 445 	446 TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 505	506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 565	566 AGGGAGCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 625	626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 685	686 TCGGTGGTCATCATGCGCCAGCTTTCATCCCCCGATATGCACCACCGGGTAAGTTCACGG 745	746 GAGACTTTAICTGACAGCGAGACGTGCCAGGGGGGATCACCATCCGTCGCCCGGGC 805	806 GIGICAATAATAICACTCTGTACAICCACAAACAGACGATAACGGCTCTCTTTTATAG 865 	866 GIGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAAGGGCGGTTCAT 925 	926 TICANTAAACCGGGCGACCICAGCCAUCCCTICCTGAITTTCCGCTTTCCAGCGTTCGGC 985	986 ACGCACACCACCCCTTCTTCTCCTTGCTTGCTTACCAGACCGGACATATTGACATC 1045 	1046 ATATATGCCTTGAGCAACTGATAGCTGTCGTCAACTGTCACTGTAATACGCTGCTTC 1105 	1106 ATAGCACACTCTTTTGACATACTTCGGGTAGTGCCGATCAACGTCTCATTTTGGCCAA 1165	1166 AAGTIGGCCCAGGGCTTCCCGGTATCAACAGGGACACCAGGATTTATTT	1226 IGAICTICCGICACAGGTAITIAITCGGCGAAAGIGCGICGGGGGAGAIGCIGCCAACITA 1285 	1286 GTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGATATGTTGT 1345	1346 GITTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATTGTATATTT 1405
ζζ QΩ	QY DP	Oy	ò d	\delta \frac{q_0}{6}	VQ Op	Qy Db	Qy Db	Qy Dp	y da	Zo a	& 43	& 8 8	δy di	රු පු	장 염	à a	da ya
QY 4381 CGCATGGGTGAGATTCCTTGAAGTTGAGTTTGGCCGTCCGCTTTACCGAAAGTTACGGG 4440 Db 17157 GGCATGGGTGAGATTCCTTGAAGTTGAGTTTGCCGTTCTACCGAAAGTTACGGG 4410	TAT			468	, ,	RESULT 5 US-10-055-001A-23	; Sequence 23, Application US/10055001A ; Publication No. US20030049835A1 ; GENERAL INFORMATION: ; APPLICANT: Wesley, Susan V.) APPLICANT: Waterhouse, Peter ; APPLICANT: Waterhouse, Peter ; APPLICANT: Helliwell, Christopher A. ; ITLLE OF INVENTION: Method and means for producing efficient silencing constructs ; ITLLE OF INVENTION: using recombinational cloning		S	; ORGANISM: Artificial sequence ; PEATURIS IN: ; OTHER IN: acceptor vector pHELLSGATE4 US-10-055-001A-23	Query Match Best Local Similarity 92.2%; Pred. No. 0; Matches 4477; Conservative 0; Mismatches 68; Indels 309; Gaps 5;	3TRARATGATATAAATATCAATATATT 85 	145 132	205	265	AAAA 325 4AAA 1342

16017 AACTGCATTTCACCAGTCCCTGTTCTGCCAAAAGAGCCGTTCATTTCAATAAACCG 16076 3301 GGCGACCTCAGCCATCCTTCTGTTTCCGCTTTCCAGCGTTCATTTCAATAAACCG 16076 16077 GGCGACCTCAGCCATCCTTCTGATTTTCCGCTTTCCAGCGTTCGGCAGCAGACGACG 16136 GGCGACCTCAGCCATCCTTCTGATTTTCCGCTTTCCAGCGTTCGACGACGAGACGACG 16136 3361 GGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTG 3420 16137 GGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTG 16196 3421 AGCAACTGATAGCTGTGACTGACAGACGAGATATTGACATCATAAGCACCTC 3480 16197 AGCAACTGATAGCTGTCAACTGTCACTGTAATAAGCGCTGCTTCATAGCACCTC 16256 3481 TTTTGACATAGCTTCTGATCAGATAACGCTGTAATAAGCGCTGCTTTAACGCTATA 3540	16257 TITITGACHACTICTTGTTCTTGAGATGATTTTCAGGACTATGACCTAGCCTAIA 16316 3541 TGAATAGGTAGTTTTTTTCACACAAAAAGAGCTCGCACCTTTTTCTTA 3600 16317 TGAATAGGTAGATTTTTTTTTCACACAAAAAGAGCTCGCACCTCTTTTTCTTA 3600 3601 TTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3661 TCCGTTTGAGAAGAACATTTGGAAGGCTGTCGGCTCGACTTGGCAGCATCACCCGGAA 3720 16437 TCCGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAA 16496 3721 GAACATTTGGAAGGCTGGTCGACTACAGGTCACTAATACCATCTAAGTTGTTC 3780 16497 GAACATTTGGAAGGCTGTCGGTCGACTACAGGTCATTAATACCATCTAAGTAGTTGATTC 3780 16497 GAACATTTGGAAGGCTGTCGGTCGACTACAGGTCATAATACCATCTAAGTAGTTGATTC 16556	3781 ATAGTGACTGGATATGTTGTTTTACAGTATTATGTAGTTCTGTTTTTTATGCAAAATCT 3840 16557 ATAGTGACTGGATATGTTGTTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCT 16616 3841 AATTTAATATTGATATTTATATATATATGTTCGTTCAGCTTTTTTGTACAAAC 3900 16617 AATTTAATATTATTATATTATATCATTTTACGTTCGTTCAGCTTTTTTGTACAAAC 16616	3901 TTGTCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCT 3960 16677 TTGTCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATTTTGCT 16736 3961 TTCAATTCTGTTGTGCACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGC 4020 16737 TTCAATTCTGTTGTGCACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGC 16796	4021 CGGTTTCGGTTCTAATGAATATATCACCGTTACTATCGTATTTTTATGAATAATA 4080	4 4 4	4261 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTAC 4320 17037 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTAC 17096 4321 GACACCGAGGGGGAACTAATAAATCTTACTGAAGGGAACTCCCGGGTTCCCGCCGGGGG 4380 17097 GACACCGAGGGGGGAACTAATAAATAACGTTCACTGAAGGGAACTCCGGGTTCCCCGCGGGGG 171097 GACACCGAGGGGGGGGGAACTCACTGAAGGGAACTCCCGGCTCCCCGCGGGGG 17156
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	15248	ACAT 1 AGTG 2 AGTG 1 AGTG 2 CCTG 2	2701 TGACGGAAGATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATCCTGGAAATAACTGTG 2701 TGACGGAAGATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGGAAGC 15477 TGACGGAAGATCACTTCGCAGAATAAATAAATACTGGTGTCCCTGTTGATACCGGGAAGC 2761 CCTGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGCAGTTCACACTTTTTTTT	1559 2880 1565 2940	2941 ATTATATTCCCCAGAACATCAGCTTAATGGCGTTTTTGATGTCATTTTGCGGTGGCTGGC	15777 AGAICAGCCACTTCTCCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATC 15836	3181 TOACTCTGTACATCCAAACAGCGATAACGGCTCTCTTTTTATAGGTGTAAACCTTA 3240 15957 TCACTCTGTACATCCACAAACAGCGATAACGGCTCTCTTTTTATAGGTGTAAACCTTA 3240 3241 AACTGCATTTCACCAGTCCCTGTTCTCGCCAGAAACAGCGCTTCTTTTTATAGGTGTAAACCTTA 1601 3241 AACTGCATTTCACCAGTCCCTGTTCTCGCCAGCAAAAAAAGAGCCGTTCATTCA

상 원	781 GGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAG 840 	& a	1861 AATATCTATACCATTACTAAATATTTTAGTTTAAAAGTTAATAATATTTTGTTAGAAT 1920
λ 20	TCCCTGT 900	% q	1921 TCCAATCTGCTTGTAATTAATGAATAAAAAATATTAAATAACAAGGGTAAAGTAACAAA 1980
දුරු පුර	TCTCGTCAGCAAAAAGGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCT 96	λο qq	1981 TAATATCAAACTAATAGAAACAGTAATCTAATGTAACAAAACATAATCTAATGCTAATGT 2040
δ, G	GTGC 102 GTGC 140	yy gy	2041 AACAAAGCGCAAGATCTATCATTTTATATAGTATTATTTTCAATCAA
Sy Db	TGTC 10 	SP DP	2101 TICTAAATAATACTTGTAGTITTAATTAACTICTAAATGGATTGACTATTAATTAAATGAA 2160
상 원	1081 AACTGTCACTGTAATACGCTGCTTCATAGCACCCTCTTTTTGACATACTTCGGGTAGTG 1140	Qy Dp	2161 TTAGTCGAACATGAATAAACAAGGTAACATGATAGATAGA
λό qα	0-0	ð fi	221
λλ G	1201 ACCAGATITALTIATICTGCGAAGTGATCTTCCGTCACAGGTATITATTCGGCGCAAAG 1260 	රු සි	2281 AGTTATCATCATCATCATAGACACAGAAATAAAGTAATCAGATTATCAGTTAAAGCTAT 2340 15267 15266
S G	STAGTT 1	cy Op	2341 GTAATATTTGGGCCATAACCAATCAATTAAAAAATAGATCAGTTTAAAGAAAG
දු පු	GCAA 1	À A	2401 CTCAAAAAATAAAAAGGGAAAAGGGTCCTAACCAAGAAAATGAAGGAGAAAAACTAGAA 2460 15267 15266
දු දු	TGTA 	දු පු	2461 ATTTACCTGCACAAGCTTGGATCCTCTAGACCACTTTGTACAAGAAAGCTGAACGAGAAA 2520
<i>장</i> 쉼	TTTT 1	& A	2521 CGTAAAATGAFATAAATATCAATATATAAATTAGATTTTGCATAAAAAACAGACTACAT 2580
oy Oy	TTGT 	දුරු පුර	2581 AATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTG 2640
% q ₀	GTAA GTAA GTAA	ර් සි	2641 ACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGCGCCGAATAAATA
Sy Db	1621 AARAATATGACAAGTGATGTGTAAGACGAAGAGATAAAAGTTGAGAGTAAGTA	<i>ò</i> ₽	2701 TGACGGAAGATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACGGGAAGC 2760
ZO QO	AATC	& A	2761 CCTGGGCCAACTTTTGGGAAAATGAGACGTTGATGGATTTCACAACTCTTATACTTTT 2820
상 음 상	TAAA 1	<i>&</i> 8	2821 CTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTACT
දු පු	ATTA 1860	& 8	2881 AAGTITCTGTAAITICTACTGTATCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGAC 2940
}	-1000 characantanatanatanatantatitititatenitahanatanatanatan 14859	ک ة 	2941 ATTIATATICCCCAGAACATCAGGTIAAIGGCGTTTTTGATGTCATTTTCGCGGTGGCTG 3000

gene silencing

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13240 ACAGCCTTCCAAAIGTTCTTCTCAAACGGAATCGTCGTATCCAGGCCTACTCGCTATIGTC 13299
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APPLICANT: Wesley, Susan
APPLICANT: Helliwell, Chris
TITLE OF INVENTION: Methods and means for monitoring and modulating still of ENVENTION: Methods and means for monitoring and modulating still between CERRENT APPLICATION NUMBER: US/10/385,546
CURRENT APPLICATION NUMBER: US 60363852
PRIOR APPLICATION NUMBER: US 60363852
PRIOR FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
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91.0%; Score 4262; Dest Local Similarity 95.6%; Pred. No. 0;
Matches 4477; Conservative 0; Mismatches
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Sequence 7, Application US/10385546
Publication No. USC030175783A1
GENERAL INFORMATION:
APPLICANT: Waterhouse, Peter
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721 ATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGGAGACGTGCACTGGCCAG

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1561 TATAATTGTGAAAAATTATTATAAATATTGTTTACATAAACAACATAGTAATGTAA 1620 Db	14859 1920 14919 1980 14979	AACAAAGGGCAAGATCTATTATATATAGTATTATTTTCAATCAA	15219 2280 15266 2340 15266	15267 15266 2401 CTCAAAAAAATAAAAAAGGGTCCTAACCAAGAAAATGAAGGAAAAACTAGAA 2460 Qy 15267 15266 Db 15267	ACAT 2

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121 ACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                      Title:
Perfect
                                                                                                                                                                                           Run on:
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Sequence 55, Appl
Sequence 31, Appl
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Sequence 21, Appl
Sequence 9, Appli
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Sequence 13, Appl
Sequence 13, Appl
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Sequence 20, Appl
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Sequence 57, Appl
Sequence 3, Appli
Sequence 55, Appli
    Sequence 24, 1
Sequence 7, April Sequence 25, 1
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Sequence 64,
5 US-10-055-001A-24
5 US-10-385-566-7
6 US-10-385-518-9
7 US-10-385-518-9
7 US-10-385-518-9
7 US-10-385-518-9
7 US-10-385-518-8
7 US-10-385-6088-55
7 US-10-356-088-55
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US-10-055-001A-26

Sequence 26, Application US/10055001A

Sequence 26, Application US/10055001A

Publication No. US20030049835A1

GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Welly Christopher A.
TITLE OF INVENTION: Weind and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT PILING DATE: 202-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1
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US-10-055-001A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence
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Matches 4682; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 6.9%; Score 323.2; DB 2; Length 416; Best Local Similarity 99.1%; Pred. No. 4.5e-60; Matches 325; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
REGINAL TYPE
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ccdB gene of plasmid pKIL 19
ATTORNEY/AGENT INFORMATION:
NAME: Altuman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMAIO.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITATAGGIGIAAACCITAAACTGCATT 886
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Job time : 204.187 secs
                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: both
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...378
OTHER INFORMATION:
US-08-379-614-3
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APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.0%; Score 325.4; DB 3; Best Local Similarity 99.7%; Pred. No. 1.5e-60; Matches 326; Conservative 0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/09/225,152A
CURRENT FILING DATE: 1998-01-04
PRIOR APPLICATION NUMBER: 08/379614
PRIOR FILING DATE: 1995-07-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITIATAGGIGIAAACCITAAACIGCA 884
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                                                                                                                                                                                                                                                                           i LOCATION: (1)...(378)
i OTHER INFORMATION: ccdB gene of pKIL 18.
US-09-225-152A-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/BE93/00051
FILING DATE: 02-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08379614 Patent No. 5910438
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                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STATE: CA
COUNTRY: U.
ZIP: 92660
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US-08-379-614-3/c
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Pred. No. 1.5e-60;
0; Mismatches 1; Indels 0
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Fatent No. 6180407
GENERAL INFORMATION:
APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
FILE REFERENCE: VANMAIO.001CP1
                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DAAS
APPLICATION NUMBER: PCT/BE93/00051
ATTORNEY/AGENT INPOMMATION:
NAME: Alteman, Daniel E
REGISTRATION NUMBER: 34,115
REPRENCE/DOCKET NUMBER: 34,115
REPRENCEY/DOCKET NUMBER: TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEPHONE: 714-760-0404
TELEFRAX: 714-760-9502
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OPERATING SYSTEM: DOS
SUCTUAREN: FASTESEQ VERSION 1.5
SUREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/379,614
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CITER INFORMATION:
US-08-379-614-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 99.7'
Matches 326; Conservative
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MOLECULE TYPE: Ge
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ORIGINAL SOURCE:
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US-09-225-152A-2/c
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US-08-379-614-2/c
; Sequence 2, Application US/08379614
; Patent No. 5910438
; GENERAL INFORMATION:
APPLICANT: Bernard, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       Score 566.4; DB 2;
Pred. No. 1.8e-111;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13854 ccedrccadcaceccecceeraacae 13827
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99.8%;
                                         : 15397 base pairs
nucleic acid
EDNESS: single
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             Best Local Similarity 99.8
Matches 567, Conservative
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                                                                                STRANDEDNESS:
                                                                                                      TOPOLOGY: li
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                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4452
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                                                                   TYPE:
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                                                                          7230 CATICIAAIGAAIAIAICACCCGIIACIAAIGHITITIAIGAAIAAIAITCICCGIICA
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7170 TGTGCACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGTT
                                                                                                                          ATTTACTGATTGTACCCTACTTATATGTACAATATTAAAATGAAAACAATATTGT
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COUNTRY: USA
ZIP: 9411-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,768
TILNG DATE: 27-UN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Joe, Lawrence K.
APFLICANT: Lee, Kathleen Y.
TITLE OF INVENTION: Delayed Ripening Tomato Plants
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REPERENCE DOCKET NUMBER: 012176-005010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGTCCAGCACGCCGGCTAACCG 4479
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APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08673768
Patent No. 5952546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bedbrook, John R. APPLICANT: Dunsmuir, Pamela APPLICANT: Howie, William J. APPLICANT: Joe, Lawrence K. APPLICANT: Lee, Kathleen Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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US-08-673-768-1/c
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12061 ATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAACC 12002
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APPLICANT: Joe, Lawrence K.
APPLICANT: Lee, Kathleen Y.
TITLE OF INVENTION: Delayed Ripening Tomato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PACENTAL RELEASE #1.0, Version #1.30 SOFTWARE: PACENTA Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,768 FILING DATE: 27-UUN-1996
*RIGH APPLICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 566.4; DB 2;
Pred. No. 1.8e-111;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE DOCKET NUMBER: 012176-005010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIPPECATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-UIN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08673768 Patent No. 5952546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%;
99.8%;
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Dunsmuir, Pamela
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TYPE: nucleic acid
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Matches 567; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunsmulr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bedbrook
APPLICANT: Dunsmir
APPLICANT: Howie, W
APPLICANT: Joe, Law
APPLICANT: Lee, Kat.
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US-08-673-768-1
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RESULT 10
5428147-1/c
; Patent No. 5428147
; APPLICANT: BARKER, RICHARD F.;KEMP, JOHN D.
; TIVENTION: OCTOPINE T-DNA PROMOTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: OCTOPINE T-DNA PRO
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/91,538
FILING DATE: 13-7UL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 40,432
FILING DATE: 11-NOV-1983
APPLICATION NUMBER: 53,786
FILING DATE: 19-NOV-1983
APPLICATION NUMBER: 144,775
FILING DATE: 06-AUG-1991
APPLICATION NUMBER: 144,775
FILING DATE: 10-ANN-1988
APPLICATION NUMBER: 144,775
FILING DATE: 10-ANN-1988
APPLICATION NUMBER: 20,78N-1983
APPLICATION NUMBER: 20,544
FILING DATE: 10-AUN-1991
APPLICATION NUMBER: 20,544
FILING DATE: 10-AUN-1991
APPLICATION NUMBER: 260,574
FILING DATE: 10-AUN-1991
APPLICATION NUMBER: 848,733
FILING DATE: 10-AUN-1991
APPLICATION NUMBER: 848,733
FILING DATE: 10-APR-1986
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FILING DATE: 26-SEP-1983
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Best Local Similarity 100.
Matches 707, Conservative
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                                                 Sequence 3, Application US/09577424

Patent No. 6525245

Patent No. 6525245

Patent No. 6525245

Patent No. 6525245

APPLICANT: Rhoads, David M

TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED I

TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS

FILE REFERENCE: UNLS90

CURRENT APPLICATION NUMBER: US/09/577,424

NUMBER OF SEQ ID MAE: 2000-05-22

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 14194;
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llarity 99.7%; Pred. No. 3.9e-142;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                      Plasmid DNA-Plasmid pZB-ALN
                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Version 1 SEQ 1D NO 3 LENGTH: 14194 TYPE: DNA TYPE: DNA SORGANIEM: Bacterial Plus-09-577-424-3
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
711; Conserv
                     RESULT 9
US-09-577-424-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4212 TATTATTACAAATCCAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTAAAAGACTGAT 4271
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                                                                                                                                      PRATURE:

NAME/KEY:

LOCATION: 3257..4315

CTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /label= 3' ccs
OTHER INFORMATION: /label= 3' ccs
OTHER INFORMATION: /label= 3' ccs
OTHER INFORMATION: 7-DNA octopine synthase gene"

FEATURE:
NAME/KEY:
LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /label= pUC18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3972 TGTGCACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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  isolate CabbB-JI
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                                                                                                                                                                                                                                                                                                                                                                                                                                        6555;
                                    NAME/KEY: -
LOCATION: 2441..3256
OTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of In5"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 709.8; DB 2;
Pred. No. 2.9e-142;
0; Mismatches 2;
    mosaic virus
  cauliflower
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.7%;
Matches 711; Conservative
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             US-09-025-583-2
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OTHER INFORMATION: //label= 3' regulatory sequence containing the OTHER INFORMATION: //label= 3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium POTHER INFORMATION: T-DNA nopaline synthase gene"
NAME/KEY: -
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LOCATION: 1608..2440
OTHER INPORMATION: /label= 3553
OTHER INFORMATION: /note= "3553 promoter sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar
OTHER INFORMATION: Bacillus amyloliquefaciens"
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LOCATION: complement (1025..1607)

OTHER INFORMATION: /label= TAA29

OTHER INFORMATION: /note= "promoter derived from the 'notes Information: /notes Tabacum"
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/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATORS SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatchouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: plasmid pVE144 (replicable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALICANEZ/ TAGENT LINCAMALION:
NAME: SVENESCO, LECORATO R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 205-8050
TELEFAX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERIFICS:
LENGTH: 6555 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (752..1024)
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LOCATION: complement (397..751)
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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LOCATION: 1..396
OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
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                                                                           LOCATION: 3257..4315
OTHER INPORMATION: /label= 3.ocs
OTHER INFORMATION: /note= "3" regulatory sequence containing the OTHER INFORMATION: /note= "3" regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium OTHER INFORMATION: T-DNA octopine synthase gene"
NAME/KEY: -
LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
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Maintenance of male-sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09025583
Patent No. 5977433
GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.7
Matches 711; Conservative
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US-08-351-413-2
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.complement (1025..1607)
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: Nicotiana tabacum"
FEATURE:
NAME/KEY: -
LOCATION: 1608..2440
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-JI"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: complement (752...1024)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene
OTHER INFORMATION: Bacillus amyloliquefaciens"
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 2441..3256
OTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of Tn5"
FEATURE:
                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGINAL SOURCE:
ORGANISM: plasmid pVE144 (replicable in E.coli)
FEATURE:
                                                                                                                                                                                             AFFLICATION NOTIBER: 05,00,00171715
FILING DATE:
RAPLICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGBYI THOORMATION:
NAME: SVENBSON, LEGORAT NUMBER: 30,330
RECERRENCE/DOCKET NUMBER: 30,330
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107050500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX:
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
"VPE: nucleic acid
"VPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TXEANDEDNESS: double
STRANDEDNESS: double
TOPOLOGY: directlar
MOLECULE TYPE: DNA (genomic)
ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME/KEY: - 2441..3256
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                                                                                                                                                                                                                                                                                                                                                                                     2333 TGTGCACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCGGTTTCGGTT 2392
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                                                                                                                             Query Match
15.2%; Score 709.8; DB 3; Length 5399;
Best Local Similarity 99.7%; Pred. No. 2.7e-142;
Matches 711; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08351413
Patent No. 5750867
GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Catchouse Road, Suite 500 East
CITY: Falls Church
  LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
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US-08-351-413-2
; Sequence 2, Api
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US-09-084-889-1
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NAME/KEY: ....1160
CUTER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from the OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: -
LOCATION: 452..1284
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the c
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OTHER INFORMATION: /note= "coding sequence of neomycine OTHER INFORMATION: phosphotransferase gene"
FEATURE:
                    GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: MONCOTYLEDONOUS PLANTS
TITLE OF INVENTION: MONCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
CUNTRY: United States
ZIP: 22313-1404
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/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 010830-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION NUMBER: 05/004,121
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-04;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-2620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5399 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/064,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: ....
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LOCATION: 1..451
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2873 TIGGIGTATGIGGGCCCCAAATGAAGTGCAGGTCAAACCTIGACAGTGACGACAAATGT 2932
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                                                                                                                                                      NAME/KEY: -
LOCATION: 2101..3160
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from the
OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4572 TGGGCGGCTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT 4624
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/label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: -
; LOCATION: 3161..5399
; OTHER INFORMATION: /Label= pUC18
; OTHER INFORMATION: /note= "pUC18 derived sequence"
US-08-475-975-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 709.8; DB 3;
Pred. No. 2.7e-142;
0; Mismatches 2;
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US-09-084-889-1
; Sequence 1, Application US/09084889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.7%;
Matches 711; Conservative
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4512
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NAME/KEY:

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2873 IIGGIGIAIGIGGGCCCCAAAIGAAGTGCAGGTCAAACCTIGACAGTGACGACAAATCGT 2932
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OTHER INFORMATION: /note= "3583 promoter sequence derived from
OTHER INFORMATION: Cauliflower mosaic virus isolate Cabbb-JI"
                                                4572 TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT
                                                                                                                                                                 US-08-45-975-1

Sequence 1, Application US/08475975

Patent No. 6002070

GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUERTING SILEGY:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,975
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/4712,975
APPLICATION NUMBER: US/08/4121
APPLICATION NUMBER: BP 90403332.1
FILING DATE: 24-MAY-1993
APPLICATION NUMBER: EP 91401848.2
FILING DATE: 32-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401848.2
FILING DATE: 08-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia
COUNTRY: United States
ZIF: 22313-1404
COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5399 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pDE108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1285..2100
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LOCATION: 452..1284
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LOCATION: 1..451
OTHER INFORMATION: ,
OTHER INFORMATION: ,
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LOCATION:
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                                                                                      Db
                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCKTION: 452..1284
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from Cauliflower mosai
OTHER INFORMATION: virus isolate Cabbb-JI"
                                                                                                                                                                                                            2332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2573 TATTATTACAAATCCAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTAAAAGACTGGAT 2632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2453 ATTTACTGATTGTACCCTACTACTTATATGTACAATATTAAAATGAAAACAATATGT
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    /label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-478-015-1
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2753 GATTCCTIGAAGITGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAAC 2812
4392 GATTCCTTGAAGTTGAGTATTGGCCGTCCTCCTACCGAAAGTTACGGGGCACCATTCAAC
                                                                                                                                                       TIGGIGIAIGIGGGCCCCAAAIGAAGIGCAGGTCAAACCTIGACAGGACAAAICGI
                                                                                                                                                                                          2873 TIGGIGIATGIGGGCCCCAAATGAAGTGCAGGTCAAACCTAGACGTGACGACGACAAATGA
                                                                            CCGGTCCAGCACGGCCGGGTAACCGACTTGCTGCCCCGAGAATTATGCAGCATTTTT
                                                                                                             CCGGTCCAGCACGCCGGGTAACCGACTTGCTGCCCCCGAGAATTATGCAGCATTTT
                                                                                                                                                                                                                                     4572 TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT
                                                                                                                                                                                                                                                                ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PROCESS FOR TRANSPORMING TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS WITHBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILLING DATE: U. -UN-1295
CLASSIFICATION: 48
PRIOR APPLICATION DATA:
APPLICATION UNMER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION UNMER: EP 91401888.2
FILING DATE: 08-UUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
FILING DATE: 23-UN-1993
ATTORNEY, AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REPERRENCE/DOCKET NUMBER: 39,300
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,015 FILING DATE: 07-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
WIDTOM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08478015 Patent No. 5712135
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5399 base pairs
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: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  circular
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MOLECULE TYPE: DN
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ZIP: 22313-1404
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ORIGINAL SOURCE:
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US-08-478-015-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /label= 3.ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from the OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
NAME/KEY: -
LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                  /label= 35S3
/note= "35S3 promoter sequence derived fro
Cauliflower mosaic virus isolate CabbB-JI"
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Pred. No. 2.7e-142;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                               /label= NPTII /note= "coding sequence of neomycine phosphotransferase gene"
                                                                                                                                                                                                  /label= pUC18
/note= "pUC18 derived sequence"
      LUFULOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.2%;
Best Local Similarity 99.7%;
Matches 711; Conservative
                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pDE108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: - 2101..3160
                                                                                                                                                                                                                                                                               LOCATION: 452..1284
OTHER INFORMATION: /1
OTHER INFORMATION: /n
OTHER INFORMATION: Ca
FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1285..2100
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                              LOCATION: 1..451
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                 NAME/KEY:
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                                                                     4195
                                                 4376 AGCATTTTTTGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACG
   1263 AAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGA
                                                                                                                                             CACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGGTTCCCCGCCGCGCG
                                                                                                                                                                                               4196 CACACCAAGCGGGGAACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCGCCGGCGCG
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                                                                                                                                                                                                                                                                                               CATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGGAAAGTTACGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                         CCATTCAACCCGGTCCAGCACGCCGGCTAACCGACTTGCTGCCCCCGAGAATTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: D'HALLUIN, Kathleen
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: BOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF ERQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: ALDRESSE: ALDRESSE: ALDRESSE: ALBRENT, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/064,121 CLASSIFICATION: 800
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APPLICATION NUMBER: EP 90403332.1
ALINGO DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILINGO DATE: 80-UUL-1991
APPLICATION NUMBER: EP 91401888.2
FILINGO DATE: 80-UUL-1991
ATTORNEY AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 35,113
REFERRICE/DOCKET NUMBER: 30,113
REFERRICE/DOCKET NUMBER: 010830-043
TELEROMONICATION INFORMATION:
TELEROMONICATION 1NFORMATION:
TELERAX: (703) 836-620
TELERAX: (703) 836-620
TELERAX: (703) 836-620
TELERAX: (703) 836-621
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08064121
Patent No. 5641664
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TYPE: nucleic acid
STRANDEDNESS: double
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US-08-064-121-1
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NAME/KEY: misc_feature
LOCATION: 1877_.2110
OTHER INFORMATION: Ontaining the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
FORTHER INFORMATION: T-DNA gene 7."
LOCATION: 2480_.3005
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: 3666..4491
COTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                                                                                                         gen
                                                                                                                                                                                                                                                             LOCATION: 1..1869
OTHER INFORMATION: /note= "Coding region of a
OTHER INFORMATION: truncated bt2 (cryIAb) gene, also designated as the bt884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4076 ATTGCGTTTTATTATTATTACAATCCAATTTTAAAAAAAGCGGCAGAACCGGTCAAACCTAA 4135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3956 CTCCGTTCAATTTACTGATTGTACCCTACTACTTATATGTACAATATTAAAATGAAAAGA 4015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCGTTCAATTTACTGATTGTACCCTACTACTATATGTACAATATTAAAATGAAAACA 4142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3776 GTCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCCTATGATGATGATGATATTTGCTTT 3835
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NAME/KEY: misc_feature
LOCATION: 5864..6541
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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LOCATION: 3006..3665
OCHER INPORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature;
COCATION: 7155._7639
COTHER INFORMATION: /note= "TR1' and TR2' promotex
COTHER INFORMATION: derived from Agrobacterium T-DNA."
                                                                                                                   ORIGINAL SOURCE:
ORGANISM: plasmid DNA designated as pJD884
                                          TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.7
Matches 730; Conservative
                                                                                                                                                                                                                              NAME/KEY: CDS
   STRANDEDNESS:
TOPOLOGY: cin
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4351
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                                           4323 CACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCCGCCGGCGCG 4382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAATCGTTGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGAC 4411
                                                                                                                                                                          4562
4052 AAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGA 4111
                                                                                              4112 cacacceacceaacraaraacerrcacreaaceaacrecaearcrecegricecegecege
                                                                                                                                              CAIGGGIGAGAITCCIIGAAGIIGAGIAIIGGCCGICCGCTCIACCGAAAGIIACGGGCA 4442
                                                                                                                                                                                                                                            CCATICAACCCGGICCAGCACGGCGGGCTAACCGACTIGCTGCCCCGAGAATIAIGC 4502
                                                                                                                                                                                                                                                                           4232 CCAITCAACCCGGTCCAGCAGCAGCGGCGGGTAACCGACTTGCTGCCCCGAGAATTATGC
                                                                                                                                                                                                                                                                                                                                                                                4292 AGCATTITITITGGTGTATATGTGGGCCCCAAATGAAGTGCAGGTCAACCTTGACAGTGACG
                                                                                                                                                                                                                                                                                                                                             4503 AGCATTTTTGGTGTATGTGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CORNELISSEN, Marc
APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCK, Jan
APPLICANT: VAN AARSSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
CORRESPONDENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 010830-049
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB 92400820.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08232016
Patent No. 5952547
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 010:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22:
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LENGTH: 7639 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4412 CTGCAGGAATTC 4423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4623 CTGCAGGCATGC 4634
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                                                                                                임
                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                        /note= "Coding region of a
truncated modified bt2 (cryIAb) gene, also designated as the
cryIAb6 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "TR1' and TR2 promoter
OTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
OTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4263 AAGACTGATTACATAAATCTTATTCAAATTTCAAAGGCCCCAGGGGCTAGTATCTACGA 4322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4203 ATTGCGTTTTATTATTACAAATCCAATTTTAAAAAAAGCGGCAGAACCGGTCAAACCTAA 4262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCGTTCAATTTACTGATTGTACCCTACTTATATGTACAATATTAAAATGAAAACA 4142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3992 Arrecertrarrarraranarceaartraaaaaaageegeagaacegraaaeeraaa 4051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3692 GTCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTT 3751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to Patent No. 595547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAATTCTGTTGTGCACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3752 CAATTCTGTTGTGCACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCG
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OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
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                                                                                                                                                                                                                                                                                                                                                                      CCATION: 2396...2921
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
FEATURE:
NAME/KEY: misc feature
          plasmid DNA designated as pPS0212
                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 3582..4407
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NAME/KEY: misc_feature
TOCATION: 5600..6457
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LOCATION: 7071..7566
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                                                                                 LOCATION: 1..1785
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
            ORGANISM:
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                                   FEATURE:
NAME/KEY:
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Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 5, Sequence 6, Sequen

Sequence

US-09-489-039A-4117 US-08-929-967-4

17, Ap Appli Appli

Sequence 4, Sequence 5,

Seguence Sequence Sequence Sequence Sequence

> US-09-272-432A-3 US-08-929-967-6

ALIGNMENTS

Sequence

US-08-929-967-5 US-08-929-967-5 US-08-811-877-3 US-08-914-916-3 US-09-272-967-6 US-09-027-169-5 US-09-489-039A-4117 US-08-929-967-4 US-08-929-967-3 US-08-850-8810-3 US-08-850-8810-3 US-08-814-817-3

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GENERAL INFORMATION:

APPLICANT: CORNELISSEN, Marc
APPLICANT: SOFTRERT, Piet
APPLICANT: SOFTRERT, Piet
APPLICANT: SOFTRERT, Piet
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANTON: PLANT CELLS
CORRESPONDENCES: 23
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CORPERSED: DOCKS ACC
COUNTRY: United States
STREET: Virginia
COUNTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-001994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTOANEY/AGENT INFORMATION:
NAME: MCGOWAN, MALCOLM K
REGISTRATION NUMBER: P39,3000
PREDEDUNYER/CONTENT NUMBER: P39,3000
                                                                                                                                                                                                                                                                                   Sequence 23, Application US/08232016
Patent No. 5952547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 936-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 7566 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 TYPE: nucleic
STRANDEDNESS:
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US-08-232-016-23
2226666666666444444
800126469786644444
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1, Appli
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12850.857 Million cell updates/sec
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4682
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Sequence 2, A
Sequence 3, A
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Sequence 6, 1
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Sequence 2,
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                                                                          8, 2004, 10:39:35 ; Search time 202.187 Seconds
                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-673-768-1
US-08-673-768-1
US-08-673-768-1
US-08-379-614-2
US-09-25-152A-2
US-09-225-152A-3
US-09-225-152A-1
US-09-225-152A-1
US-08-961-527-70
US-08-961-527-70
US-08-961-527-70
US-08-56-978B-78
US-08-56-978B-78
US-08-56-978B-78
US-09-630-929-4
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-232-016-23
US-08-232-016-22
US-08-64-121-1
US-08-478-015-1
US-08-08-15-97-1
US-09-084-889-1
US-09-575-1413-2
US-09-577-424-3
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                                                                                                                                                                                                     682709 segs, 277475446 residues
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                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    - nucleic search, using sw model
                                                                                                                                                                   IDENTITY_NUC Gapop 10.0 , Gapop 10.0
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Maximum DB seq length: 200000000
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Match Length DB
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1808	<u>AAATAAATAAATAATATTTTTTTTAATAATAGTTTAT</u>
15016	
186	TACCATTACTAAATATTTTAGTTTAAAAGTTAAATAATATTTTGTTAGAAATTCCAATC 192
D 0	AITAITIGITACITITAGCITGITAITITAATATITITGITITATIGADAATTACAAG 149:
14928	aacaagci rttaaaci
198	AACAAAACATAATCTAATGCTAATATAACAAAG 204
96	
2048	ATTAATTTCTAAA 2
2108	ATACTIGIAGITITIATTAACTICTAAATGGATTGACTATTAATTAAATGAATTAGTCG 216
2168	CATGAATAAACAAGGTAACATGATAGATCATGTCATTGTGTTATCATTGATCTTACAT 2227
. 53	aaaacaaatattaatgctagtatatcatcttacatgttcgat
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228	CATCATCATAGACACACGAAATAAAGTAATCAGATTATCAGTTAAAGCTATGTAATAT 2347
4	TTACACATCACTTGTCATATTTTTTACATTACTATGTTGTTTATGTAAA
2348	TTGCGCCATAACCAATTAAAAAATAGATCAGTTTAAAGAAGATCAAGGCTCAAAA 2407
2408	BARARIGAAGGAGAAAACTAGAAATTTACC 246
2468	aaaacgtaaaa 252 gaaacgtaaaa 144
2528	TGATATAAATTATATATATTATAATTAGATTTTGCATAAAAAGAGACTACATAATACTG 2587
2588	TAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTA 2647
2648	L 4
2708	TGTTGATACCGGGAAGCCCTGGGC
2768	AATGAGACGTTGATCGGATTTCACAACTCTTATACTTTTCT
2828	AGCCTCTATACTTACTAAAGGTGATAAAGTTTC
2888	TATCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTG 2938

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                                                                                                                                                                                                                                               GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGGC
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                                                                                                                                                           GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGGC
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selectable marker region capable of being expressed in the recipient cell
; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
ce region capable of being recognized by RNA polymerases of a eukaryotic
cell or by prokaryotic RNA polymerases; (ii) first, second, third and
colyademylation region functional in the eukaryotic cell. The first and
colyademylation region functional in the eukaryotic cell. The first and
control recombination sites, or the eukaryotic cell. The first and
courth recombination sites, or the same recombination site, and preferably
are capable of reacting with a same recombination site, and preferably
care identical. The first and second recombination site, or the third and
cfourth recombination sites, do not recombine with each other or with a
capable stranded RNA which can be used for silencing large amounts
cc double-stranded RNA which can be used for silencing large amounts
cc acid sequences. The vectors can also be used to convert a DNA fragment
into an inverted repeat structure. Plants transformed with a vector from
correspond to the present invention can be used in a conventional breeding scheme to
convert produce more plants with the same characteristics or to introduce a
chimeric gene for reduction of the phenotypic expression of nucleotide
canners from the present sequence represents an acceptor vector nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                               sequence from the present invention
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b)

Claim 15; Page 74-83; 104pp; English.

silencing tar stranded RNA

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                          CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA
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                                                               AGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTT
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid comprising one or more recombination sites with a target the first population to recombine with the first target nucleic acid molecules of molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to or all of the nucleic acid molecules of the second population to frecombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolatang nucleic acid molecules. The present sequence represents the destination plasmid pDONNE212(R) nucleotide sequence
                                                                                                                                    Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
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Byrd DRN;
Esposito D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAATAAGAAAAAGAGGTGCGAGCCTCTT
                                                                                                                                                                                                                                                                                Disclosure; Fig 29B-C; 273pp; English
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of mucleic acid, cb) causing some or all of the nucleic acid molecules of mucleic acid for a second population, (c) mixing the second population of nucleic acid, and (d) causing some of nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to recombine with some or all of the second target nucleic acid molecules to selecting and isolating nucleic acid molecules. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONN212(F) nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTAGATTTTGCATAAAAAAAAGACTACATAATACTGTAAAACACAAACATATCCAGTC 145
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recombination; nucleic acid selection;
ds.
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23.5%; Score 1102.4; DB 7
Best Local Similarity 99.5%; Pred. No. 2.2e-147;
Matches 1106; Conservative 0; Mismatches 6;
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nucleic acid isolation;
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of molecules to form a second population, (c) mixing the second population of nucleic acid with a second population, (c) mixing the second population of nucleic acid with a second target nucleic acid, causing some or all of the nucleic acid molecules of the second population to or all of the nucleic acid molecules of the second population to from a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR212 nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid insertion, recombination, nucleic acid selection, nucleic acid isolation; ds.
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                                     4403 ATAGCACACTCTTTTTGACATACTTCGGGTA 4372
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1106 ATAGCACACCTCTTTTGACATACTTCGGGTA
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Matches 1106; Conservative
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from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting c gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, c changing copy number, changing replicons, cloning into phages and cloning. (I), (III), (III), host cells and vectors can be used in the coduction of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
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5304 5244 5184 5064 4884 4644 5424 5364 5124 5004 4944 4824 4764 4704 ö 865 145 205 265 325 385 445 505 565 625 685 745 805 GIGIAAACCITAAACTGCATITCACCAGICCCTGITCTCGTCAGCAAAAGAGCCGITCAI 925 82 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATTATCAATATATT 5123 ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA AGGGAGCCTGACATTTATATATTCCCCAGAACATCAGGTTATATGGCGTTTTTTGATGTCATTT GIGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTTTATAG AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTC AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACACATATCCAGTC ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA **AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTGTGTGACAAAATAAAAACATCTACCT** ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 5063 TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTATA 566 AGGGAGCCTGACATTTATATTTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCCGATAACGGAGACCGGCACACTGGCCATA TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGG GAGACTITATCTGACAGCAGACGTGCACTGGCCAGGGGATCACCATCCGTCGCCCGGGC GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGGC GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTTTATAG ., Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 U; 0 Other; DB 3; Length 5584; Indels 2.7e-148; Score 1108.8; 0; Mismatches Pred. No. 23.7%; 99.8%; Conservative Best Local Similarity Matches 1110; Conserv 5483 5423 5363 5303 566 5243 326 386 5003 4943 4763 4703 26 146 5183 4823 746 98 1883 686 908 Query Match 206 446 909 626

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GEGTABARCCTTABARCTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCGCGTTCAT
                                                                                                                                                                                                            4463 ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC
                                                 TTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTTTCCGGCTTTCCAGCGTTCGGC
                                                                        TTCAATAAACCGGGGGGACTCAGCCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGC
                                                                                                               ACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1108.8; DB 7;
Pred. No. 2.7e-148;
0; Mismatches 2;
                                                                                                                                                                                                                                                                         ATAGCACACCTCTTTTGACATACTTCGGGTA 4372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Donor plasmid pDONR207 nucleotide sequence.
                                                                                                                                                                                                                                              ATAGCACACCTCTTTTGACATACTTCGGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 18B-C; 273pp; English.
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99.8%;
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Best Local Similarity 99.8
Matches 1110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insertion;
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nucleic acid
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att recombination site. (I), (II), primers, vectors and methods from the present invention are used for the recombinational cloning of mucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (I), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                    Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                         DB 3; Length 4939;
                                                                                                                                                                                                                                                                                                                                    Score 1108.8; DB 3;
Pred. No. 2.7e-148;
0; Mismatches 2;
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4415 GIGHTHIN GENERAL CACTURE CACARACAGACA CANA CACTURE TATATAGE 4475 3815 ATTCATATACGCTAGTGTCATAGTCCTGAAATCATCTGCATCAAGAACAATTCACAAC 4055 TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCACCTGGATTTTCAGCCTCTATACTTA 4115 AGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 4235 redecedence de la contrata del contrata de la contrata del contrata de la contrata del contrata de la contrata del contrata de la contrata del contrata del contrata de la contrata de la contrata de la contrata de la contrata de la contrata de la contrata del contrata del contrata de la contrata del contr TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGG 4355 3816 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 3875 3995 3636 GCCAACTTTGTACAAAAAGCTGAACGAAAACGTAAAATGATATAAATATCAATATATT 3695 3696 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACCACAACATATCCAGTC 3755 805 865 685 745 265 325 385 445 565 145 205 TCTTAIACTTTTCTCTTACAAGICGTTCGGCTTCAICTGGAITTTCAGCCTCTATACTTA 505 AGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 625 85 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCCGATAACGCAGACCGGCACACTGGCCATA GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTTTATAG CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA GAGACTTTATCTGACAGCAGGCGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGGC TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGGATATGCACCACCGGGTAAAGTTCACGG GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGATCACCATCGGTCGCCCGGGC ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA **ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC** GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATTATCAATATATT <u>AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTC</u> Gaps ·; Indels 23.7%; ilarity 99.8%; Conservative (Best Local Similarity Matches 1110; Conserv 3996 4116 266 4176 4236 4296 386 446 4056 4356 908 326 506 626 989 746 56 146 206 266 86

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1002 TTCAATAAACCGGGGGACCTCCAGCCATCCCTTCTGATTTTTCCGCTTTCCAGCGTTCGGC
                                                                                                                                    ACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC
                                                                                                                                                                ACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGGAGATATTGACATC
                                                                                                                                                                                                  ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC
           GTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCAT
                                       942 GIGIAAACCITAAACIGCATITCACCAGICCCIGITCICGICAGCAAAAGAGCCGITCAI
                                                                         TICAATAAACCGGGCGACCICAGCCATCCCTTTCCTGATTTTCCGCCTTTCCAGCGTTCGGC
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99US-0126049P.
99US-0136744P.
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                                                                                                                                                                                                                                                                                                           102 GCCAACTTTGTACAAAAAGCTGAACGAAACGTAAAATGATATAAATATCAATATTT 161
                                                                                                                                                                                                                                                                                                                                           AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATTCCAGTC 145
                                                                                                                                                                                                                                                                                                                                                               162 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACAACATATCCAGTC 221
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                                                                                                                                                                                                                                                                               85
                                                          The invention comprises a method for moving an insert nucleic acid molecule between vectors, the method involves moving an insert nucleic acid from one vector to another using site-specific recombination. The method of the invention is useful for studying the biology of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA
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                                                                                                                    organism, including array construction, reporter gene fusions, mutagenesis, protein production and characterisation. The present DNA sequence represents the plasmid vector pMK2010 of the invention.
                                                                                                                                                                                                                                                                               GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATTTCAATATATT
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                     Sequence 4892 BP; 1277 A; 1157 C; 1097 G; 1361 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                  8; Length 4892;
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Pred. No. 2.7e-148;
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                             41; Page 47-51; 52pp; English.
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99.8%;
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Best Local Similarity
protein production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage lambda; att; recombination site; attB; attR; attL; attL; mutant; recombinational cloning; entry vector; destination vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising a second recombination site that interacts with the mutated
1122 ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant; recombinational cloning; entry vector; de gene product targeting; fusion tag cleavage; ds.
                                                                                                            ATAGCACACCTCTTTTGACATACTTCGGGTA 1137
                                                                                                                                                                                              ATAGCACACCTCTTTTTTTTTTTTTTTTTCGGGTA 1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donor plasmid pDONR205 nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site-specsific recombination; array construction; reporter gene fusion;
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AGGAGCCTGACATTTATATTTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT
                                                                                      TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCCGATAACGGAGACCGGCACACGCCATA
                                                                                                                                                                                                                                                                                    GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTTTATAG
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                                                         TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGGATAACGGAGACCGGCACACTGGCCATA
                                                                                                                                                                                                           GAGACITITATICIGACAGAGGAGGACGIGGCCAGGGGGATCACCATCCGTCGCCCGGGC
                                                                                                                                  TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAGCACACCTCTTTTGACATACTTCGGGTA 1137
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                                                                                                                                                                                                                                                                                                                        The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, comprising some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population, (b) mixing the second population of nucleic acid with a second molecules of the second population to recombine with population to all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence
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                                                                                                                                                                                                               Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents the destination plasmid pDONR201 nucleotide sequence
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Matches 1110; Conserv
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942 GIGIABAACCTIAAACIGCATITCACCAGICCCIGITCTCGTCAGCAAAAGAGCGCITCAI
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                                                                                              ATTCATATACGCTAGTCTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, and attB2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising as second recombination site that interacts with the mutated comprising a second recombination site that interacts with the mutated from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting concluding notion intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules, constructing genes for fusion proteins, crequinces, constructing genes for fusion proteins, crequinces, constructing genes for fusion proteins,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          changing copy number, changing replicons, cioning into phages and cloning. (II), (III), host calls and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
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Matches 1110; Conservative
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gene for reduction of the phenotypic expression of nucleic he present sequence represents an acceptor vector nucleotide from the present invention:	25.8%; Score 1208.4; DB 6; Length 17681; Similarity 60.4%; Pred. No. 2e-162; 4; Conservative 0; Mismatches 1476; Indels 80;	CTCGAGACAAGTTTGTACA 	1 ATATTAAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATACTCT	CAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGAC	1 CCAAATGITCITCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGITCTT	1 CTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCA 	1 TRAAAAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTGTGTGACAAAATAAAAACATC 	TACCTATICATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTCC 	ACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTAT	ACTTACTAAACGTGATAAAGTTTCTG	2 GCTATCAGTTGCTCAAGGCATATATGATGATGTCAATATCTCCGGTCTGGTAAGCACAACAT 1 GTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGT 1		CALTITUGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1 CCATATCGGTGGTCATGCGCCAGCTTTCATCCCCGGATATGCACCACGGGTAAAGTT	1 CACGGGAGACTTTATCTGACAGCAGGACGTGCACTGGCCAGGGGGGGAGATCACCGTCGGTCG		1 rescensiscacenciscisciscasataassiciscossaaacitiacessissassis	TATAGGIGTAAACCITAAACTGCATTICACCAGTCCCTGTTCTCGTCAGCAAAA	5 GAGCCGTTCATTTCAATAAACCGGGGAACTCAGCATCCTTTCCTGATTTTCCGCTTTC	1 TCGGGGAAGAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACC
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter cell or by prokaryotic ENA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and courth recombination sites; (iii) 3' transcription terminating and courth recombination sites, or the second and third recombination sites, or the second and third recombination sites, or the second in the combination sites, and second recombination site, and preferably are identical. The first and second recombination site, and preferably are identical. The first and second recombination site, or the third and same recombination sites, or he to recombination site, and preferably of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerases (ii) first, second, third and fourth recombination sites; (iii) 3 transcription terminating and fourth recombination sites; (iii) 3 transcription terminating and fourth recombination sites, or the second and third recombination sites are identical. The first and second recombination sites, are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombination sites, or the third and court recombination sites. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing a target nucleic of double-stranded RNA which can be used for silencing a farget mucleic.
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Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.
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Local Similarity 95.0%;
nes 4449; Conservative
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15459	16575 ATRICHANTATION OF THE TRANSPORT OF THE TRANSPORDANCE 16694	ABQ82142 DD ABQ82142 standard; DNA; 17458 BP. XX AC ABQ82142; XX DT 11-DEC-2002 (first entry) XX DT ACCEPTOR VECTOR PHELLSGATE 11 nucleotide sequence SEQ ID NO:25. XX
CCTGGGGCGAACTTTTGGCGAAATGAACGGTTGATGGGTTGATGGGTTGATGGGGAAGGGGGGAAGGGTGGAAGGGTGATGGTGATGGTGTTGATGTGAAAGGTGATTTTTGGGGTGATGA	印格 配格 配格 配格 配格 印格 印格 印格 印格 印格 印格 印格 印格 印格 印度 四十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二十二	RESS ABQ AC XX XX XX YX YX XX XX
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The present invention describes a vector (1) comprising operably linked CC DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coll; (b) selectable marker region capable of being expressed in the recipient cell coll capable of being recognized by RNA polymerases of a enkaryotic cell or by prokaryotic RNA polymerases; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and fourth recombination functional in the eukaryotic cell. The first and coll polyademylation region functional in the eukaryotic cell. The first and coll properties of the combination sites are identical. The first and second recombination sites, or the second and third recombination sites, or the second recombination sites, or the third and coll courth recombination sites, do not recombination sites, or the third and coll coll coll coll capable of the vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target mucles of double-stranded RNA which can be used for silencing target mucles caping the present invention can be used in a conventional breading scheme to the present invention can be used in a conventional breading scheme to chimeric gene for reduction of the phenotypic expression of nucleic collection from the present sequence represents an acceptor vector nucleotide called and a collection for nucleotide capables.
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                            New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA.
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                                                                                                                                   Claim 15; Page 74-83; 104pp;
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Matches 4477; Conservative
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      TICICCGITCAATITACIGATIGIACCCIACITAIAIAIGIACAAIAITAAAAIGAAAA
                                                                                  CAATATATTGTGCTGAATAGGTTTATAGGGACATCTATGATAGAGGGCGCCACAATAACAA
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cc fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably creed identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic closed sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimmeric gene for reduction of the phenotypic expression of nucleic capacity. The present sequence represents an acceptor vector nucleotide sequence from the present invention
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	ACGATAACGGCTCTCTTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGT ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGT
	TCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGGGACCTCAGCCATCCCTTCCTT
	961 GATTTTCCGCTTTCCAGCGTTCGGCACGCAGGCGTCGTTCTATTCTGCATGGTTGTGC 1020 13960 GATTTCCGCTTTCCAGCGTTCGGCACGCAGGCTTCATTCTGCATGGTTGTGC 14019
	TTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTC
	AACTGTCACTGTAATACGCTGCTTCATAGCACCTCTTTTTGACATACTTCGGGTAGTG
	ACGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGGTACTCAACGGGCCCAGGGCTTCCCGGGTATCAACAGGGGCCCAGGGCTTCCCGGGTATCAACAGGGGCCCAGGGCTTCCCGGGTATCAACAGGGGACAAAGTTGGCCTTCCCGGGTATCAACAGGGGCCCAGGGCTTCCCGGGTATCAACAGGGGACAAAAGTTGGCCTTCCCGGGTATCAACAGGGGACAAAAGTTGAAAAGTTGCAAAAAGTTGAAAAAAAA
	ACCAGGATTATTATTCTGCGAAGTGATCTTCGCCAGGGTTTATTATTCGGCGCAAAG
	ACCAGGATITATITATICIGCGAAGTGATCTICCGTCACAGGTATTTATTATCGGCGCAAAG TGCGTCGGGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTT
	TGCGTCGGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTT
	GATTCATAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTTATGCAA
	AATCTAATTTAATATATGGTATTTATATCATTTTACGTTTCCGGTTCAGCTTTCTTGTA
	CAAAGTGGTCTCGAGGAATTCGGTACCCCAGCTTGGTAAGGAAATAATTTTTTTT
	CAAAGIGGICICGGAGGAATICGGIAACCCCAGCTIGGIAAGGAAATAATATATTTTTTT TCCTTTTAGTATAAAAAAAAGAGAAGTGATGTTAATTAGTATGATATAAAAAA
	TCCTTTTAGTATAAATAGTTAAGTGTTAATTAGTTATTATTAT
	TATAATTGTGAAAAAATAATTTTATAAATATTTGTTTACATAACAACAACATAGTAATGTAA
	AAAAATATGACAAGTGATGTGTAAGAAGGAGGAAGATAAAAGTTGAGAGTAAGTTATAT
	TITITAATGAATITIGATGGAACAIGTAAGATGATAATACTAGCATTAATATTTGITITAATC
	TITIAATGAAITTGAICGAACAIGIAAGAIGAIAIACIAGCAIIAAIAITTGITITAAIC
	ATAATAGTAATTCTAGCTGGTTTGATGAATTAAATATCAATGATAAAATACTATAGTAAA
	AATAAGAATAAATAAATAAATAATAATATTTTTTTTATGATTAATAGTTTTATTA
	800 AATAAGAATAAATTAAAATAATATTTTTTTTTTATGATTAATATTTTTT
	1861 AATATCTATACCATTACTAATATTTTAGTTTAAAAGTTAATATATTTTGTTAGAAAT 1920

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Copyright (c) 1993 - 2004 Compugen Ltd.
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IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6747726 Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues Searched:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

Description	Abq82143 Acceptor		-				Abz58767 Destinati	Ada50329 Plasmid v		Aac55632 Donor pla		Abz58768 Destinati	Abz58769 Destinati	Abz58770 Destinati	Abg82141 Acceptor						- 54	Add44386 Flaveria	Aaq40419 Sequence
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% Query Match	100.0	91.0	89.7	68.3	25.8	23.7	23.7	23.7	23.7	23.7	23.7	23.5	23.5	23.5	23.0	22.9	21.1	20.5	17.7	17.6	16.7	16.7	16.0
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ALIGNMENTS

ABQ82143 standard; DNA; 17681 BP (first entry) 11-DEC-2002 ABQ82143; RESULT 1 ABQ82143

Acceptor vector pHELLSGATE 12 nucleotide sequence SEQ ID NO:26.

Chimeric nucleic acid construct, recombinational cloning; silencing, recombination site; double stranded RNA; plant; ds.

Synthetic.

WO200259294-A1. 01-AUG-2002. 24-JAN-2002; 2002WO-AU000073.

26-JAN-2001; 2001US-0264067P. 29-NOV-2001; 2001US-0333743P.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

Helliwell C; Waterhouse P, Wesley S,

WPI; 2002-682669/73.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA.

Claim 17; Page 93~102; 104pp; English.

The present invention describes a vector (I) comprising operably linked by fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli, (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polygadenylation region functional in the eukaryotic cell. The first and

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4203 ATTGCGTTTTATTATACAAATCCAATTTTAAAAAAGGGGCAGAACCGGTCAAACCTAA 4262
                                                                            3992 ATTGCGTTTTATTATAAAAATCCAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTAA 4051
                                                                                                                                                 4052 AAGACTGATTACATAAATCTTATTCAAATTTCAAAAGCCCCCAGGGGCTAGTATCTACGA 4111
                                                                                                                                                                                                4323 CACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCCGCCGCGCG 4382
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                                                                                                                                                                                                                                                                                             CCATTCAACCCGGTCCAGCACGGCGGCTAACCGACTTGCTGCCCCGAGAATTATGC 4502
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Search completed: May 9, 2004, 11:29:16 Job time : 11671.2 secs

Db 8472 TGCGTTTTATTACAAATCCAATTTTAAAAAAAGGCGCAGAACCGGTCAAAAC 8413 Qy		4505 CATITITITIGEOGREGOCCCCAATGAGTGCAGGTCAAACCTTGACAGTGACGACTAACAGGCGACTAATGAGTGTAACTGACGACTGAACCTTGACAGTGCACGACGACGACGACGACGACGACGACGACGACGACGAC		RESULT 15 A24783 LOCUS DAPA 11near PAT 24-FEB-1995 LOCUS DEFINITION Plasmid pPS0212 replicable en E.coli. ACCESSION A24783 VERSION KEYWORDS SOURCE Synthetic construct ORGANISM synthetic construct Artificial sequences. REFRENCE 1 (bases 1 to 766)	ORS E MODIFIED NAL Patent: W	Source 17566
AUTHORS Kardailsky, I. and Weigel, D. TITLE Direct Submission JOURNAL Submitsed (17-SEP-1999) Plant Biology Laboratory, The Salk JOURNAL Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA. FEATURES Location/Qualifiers 1. 10138	<pre>misc_feature //db_xret="taxon:109189" misc_feature 35204 misc_feature 22052662 misc_feature //note="dervied from pUC19" misc_feature //note="dervied from phage f1" misc_feature 22052662 misc_feature 22052662</pre>		_reature _feature	mXNA complement (48791. 9342) CDS COMPLEMENT (8791. 9342) / note="promotes resistance to glutamine synthetase inhibitors" / note="promotes resistance to glutamine synthetase inhibitors" / codon state="1" / transl table=11 / protein id="AAF15587.1" / db_xref="G1:6537290" / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIRRATEADMPAVCTIVNHYIETSTVNFRTEPQEPQ / translation="MSPERREADIR" / translation="MSPERREA	<pre>mRNA complement(942110119) /product="mannopine synthase" /note="5" end and promoter"</pre>	Query Match 15.7%; Score 735; DB 12; Length 10138; Best Local Similarity 100.0%; Pred. No. 2.2e-96; August Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 3905 CTAGAGTCCTGCTTTAATGAGATATGCGAGACGCTATGATCGCATGATATTGCTTTCA 3964 Db 8772 CTAGAGTCCTGCTTTAATGAGATATGCGACGCTATGATCGCTTGCTT

4062 TICACTITICCGGNNNNCTCTAGAGTCCTGCTTTAATGAGATATGCGGAGACGCCTATGATGTC 412	Db 4122 GCAIGATATTGCTTTCAATTCTGTTGTACAGAAACCTGAGCATGTAGCT 4006	QY 4007 CAGATCCTTACCGCTTTCGTTCTAATGAATATCACCGTTACTATT 4066 Db 4182 CAGATCCTTACCGCCGCTTTCGGTTCATTCTAATGAATATATCACCCGTTACTGTAT 4241			4362 GCGCAGATAACAAAGAGTGCGTTTTATTATTACAAATCCAATTTCAAAAAGCGGCAG 44 4247 AACCGGTCAAAAGAGCGGTTTAATAATAAAAATTCCAATTTCAAAAGGCCCCAG 43	4422 AACCGGTCAAAACTAATTACATAAATTTCTATTCAAATTTCAAAAGGCCCCAG 4307 GGGCTAGTATTCTAGACACACGAGGGGGGGAACTTAATAAAGGAACTCCG	Db 4482 GGGCTAGTATCTACGACACGCGGGCGGACTAATAACGTTCACTGAAGGGAACTCCG 4541 Qy 4367 GTTCCCGGCGGGGGGGAAGTAGAATTGAAGTTGAGGTTGAGGTTCACTGAAGGGAACTCCA 426	Db 4542 GTTCCCGCCGGCGCATGGGTGAGTTCCTTGAAGTTGAGTGTTGAGTGTCGTCCGTC	Db	4547 AACCTIGACAGAACCAAATCGTIGGGGGGGGGGGGGGATTTTGCGACACATGT 46 4722 AACCTIGACAGTGACGACAAATCGTIGGGCGGGGCGAATTTTGCGACAACATGT 46 4607 CGAGGCTCAGCAGACAAATCGTIGGGCGGGCGGGCGGAATTTTGCGACAACATGT 47 4607 CGAGGCTCAGCAGGACCTGCAAGCTAG 4641 4782 CGAGGCTCAGCAGGACCTGCAAGCTTG 4816	RESULT 14 AR187951/c LOCUS LOCUS DEFINITION Activation-tagging vector pSKI015, complete sequence. ACCESSION AF187951 VERSION AF187951 VERSION AF187951. GI:6537289	ALTWORDS SOURCE Activation-tagging vector pSKI015 ORGANISM Activation-tagging vector pSKI015 artificial sequences; vectors. REFERENCE 1 (bases 1 to 10138)		TITLE Activation tagging in Arabidopsis JOURNAL Plant Physiol. 122 (4), 1003-1013 (2000) MEDLINE 20223715 PUBMED 10759496 REFERENCE 2 (bases 1 to 10138)
OY 1712 ATATACTAGCATTAATATTTGTTTTAATCATAATAGTAATTCTAGCTGGTTTGATGAATT 1771 Dh 8132 ATATACTAGCATTAATATTTGTTTTAATCATAATAGTAATTCTAGCTGGTTTGATGAATT 1771	1772 AAAIATCAATGATAAATACTATAGTAAATAAGAATILCIAGCIGGIIIGAGTA 1181 1772 AAAIATCAATGATAAAATACTATAGTAAAATAAGAATAAATAAA	8192 AAATATCAATGATAAATACTATAGTAAAATAAGAATAAATA	Db 8252 TITATGATTAATAGTTTATTATAATAATATCTATACCATTACTAAATATTTTAGTT 9311 Qy 1892 TAAAAGTTAATAAATATTTTTGTTAGAAATTTCCAATCTGCTTGTAATTATCAATAACAA 1951 Db 8312 TAAAAGTTAATAATAATAATAATAATAATAATAATAATAA	1952 ANTAITAANTACAAGTAAGTAACAATAATAACAACTAATGAACGAACAGAATTAA 1111111111111111111111111111111	2012 TGTAACAAAACATAATGCTAATATAACAAAGCGCAAGATCTATCATTTATAAGAAGA32 TGTAACAAAAAGATGATTTATATAGAAAGCGCAAGATCTATCATTTATATAGAAGACGCAAGATCTATCATTTTATATAGAAGACCAAAGACCTAATATTATAACAAAAGCGCAAAGATCTATCATTTTATATAGA	QY 2072 TATTATTTTCAATCAACATTCTTAATAATAATAATACTTGTAGTTTTATTAACTT 2131	QY 2132 CTAAATGGATTGACTATTAATTAAATGAATTAGTCGAACATGAATAAACAAGGTAACATG 2191 	2192 ATAGATCATGTCAT 		RESULT 13 A23998 LOCUS LOCUS DEFINITION PIE4 expression vector. DEFINITION A23998 VERSION A23998 VERSION A23998 CESTON A23998 CESTON A23998 COURCE SOURCE SO	AUTHORS Nazarov, V., Botterman, J., Stanssens, P. and Sevcik, J. TITLE A novel ribonuclease and its inhibitor JOURNAL Patent: EP 0537399-A 3 21-APR-1993; FRATURES Location/Qualifiers	or/ db/	Ouery Match Best Local Similarity 94.6%; Pred. No. 4.4e-98; Matches 771; Conservative 0; Mismatches 44; Indels 0; Gaps 0;	OY 3827 IITAIGCAAAAICTAAITIAAIAITGAIAITAIAICAITIAGGITTACGITCAGC 3886

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8011
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RIKVMANAADTPRDALPARNCARQGIGLCKTEHMFFASDERIKAVRKUIMAVTPEORKV
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9737. 9972, 10177. 10305, 10401. 11559, 11673. 11811,
11897. 12074, 12255. 12424, 12514. 12642, 12721. 12858,
13102. 13179, 13557. 13648, 14222. 14264)
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pdk gene; pyruvate, orthophosphate dikinase.
Flaveria trinervia
Flaveria trinervia
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                              1 (bases 1 to 14645)
Rosche, E., Streubel, M. and Westhoff, P.
Primary structure of the photosynthetic pyruvate orthophosphate
dikinase of the C3 plant Flaveria pringle; and expression analysis
of pyruvate orthophosphate dikinase sequences in C3, C3-C4 and C4
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9324. 9486,973. 9972,10177. 10305,10401. 10580,
10735. 10872,10947. 11111,11221. 11382,11480. 11569,
11673. 11811,11897. 12074,12295. 12424,12514. 12642,
12721. 12858,13102. 13179,13557. 13648,14222. >142643,
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join(1212. 1346,1481. 1733,7839. 7895,9093. .9230,
9324. .9486,9737. .9972,10177. .10305,10401. .10580,
10735. .10872,10947. .11111,11221. .11382,11480. .11569,
11673. .11811,11897. .12074,12295. .12424,12514. .12642,
12721. .12888,13102. .13179,13557. .13648,14222. .5142641,
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9737. 9972,10177. 10305,10401. 10580,10735. 10872,
10947. 11111,11221. 11382,11480. 11569,11673. 11811,
11897. 12074,12295. 12424,12514. 12642,12721. 12858,
13102. 13179,13557. 13648,14222. 14264)
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Molekular-, biologie der Pflanzen, Heinrich-Heine-Universitaet,
Universitaetsstr. 1, 40225 Duesseldorf, FRG
Location/Qualifiers
              for pyruvate, orthophosphate dikinase.
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/organism="Flaveria trinervia"
/organism="Flaveria trinervia"
/mol_type="genomic DNA"
/clone="inFtrpdk, inFtrpdkA-F"
/tissue type="full expanded leaves"
/clone_lib="lambda Dash, lambda ZAPII"
|212. .14264
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/gene="pdk"
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Rosche, E.
              trinervia pdk gene
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Location/Qualifiers
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Artificial Sequence: intron 2 of the Flaveria trinervia CC puryvate orthophosphate dikinase FH Key 1.784 Tordaniam-/Artifiers FT source //ordaniam-/Artifiers //ordaniam-/Artifiers //ordaniam-/Artifiers //ordaniam-/Artifiers
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ilarity 100.0%; Pred. No. 1.2e-102;
Conservative 0; Mismatches 0;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/gene="pdk" /EC_number="2.7.9.1"

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4544 ATAATAATATAGTTGTTATAATTGTGAAAAAATAATTATAAATATATTTGTTTACATAAA 4603
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SM synthetic construct
artificial sequences.

E 1 (bases 1 to 786)
S Waterhouse, P.M., Wang, M.B. and Graham, M.W.
Method and means of obtaining improved phenotype
L Patent: JP 2002511258-A 7 16-APR-2002;
COMMONMEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
OS Artificial Sequence
PN JP 2002511258-A/7
PD 16-APR-2002
PF 07-APR-1999 JP 2000543598
PF 07-APR-1999 US 09/056767,03-AUG-1998 US 09/127735 PI
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PR 08-APR-1999 US 09/056770,03-AUG-1998 US 09/127735
PETER MICHAEL WALERHOUSE, MIN BO WANG MICHAEL WALN GRAHAM PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00,C C Describti
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Method and means of obtaining improved phenotype.
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BEDGSPEKIT IELYABGCIRLFHBIDISDPCPYTWSLDSRLABELDYLLMNDLADVDCENWE
EDTPFKDPRELYDFKTEKPBEELVBSHGDLGDSNIFWCDGKVSGFIDLGRSGRADKW
YDIAPCVRSIREDIGBEQYVELPFPDLLGIKPDWEKIKYYILLDELF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MAKMRISPELKKLIEKYRCVKDTEGMSPAKVYKLVGENENLYLK
                                                                                                                                                                                                                                                                                                                                                              /note="pHANNIBAL is a derivative of cloning vector pART7 which was a derivative of pGEM-92f(-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1425 GTTCAGCTTTCTTGTACAAAGTGGTCTCGAAGAATTCGGTACCCCAGCTTGGTAAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                Industry,
AUSTRALIA
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Pred. No. 3.1e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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/note="octopine esynthase (ocs) terminator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
transT_table=11
product="kanavin resistance protein"
protein_id="CAC86251.1"
db_xref="GI:15982217"
                                                                                   Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5288. .6053
/organism="Agrobacterium tumefaciens"
/mol.type="other DNN"
/mb xref="taxon:358"
                                                                                                                                                                                                                       /organism="Cloning vector pKANNIBAL"
/mol_type="cother DNA"
/db_xref="taxon:167048"
/lab_host="Bscherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mosaic virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4493. .5234
/organism="Plaveria trinervia"
/mol_type="other DNA"
/db_xref="taxon:4227"
                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Escherichia coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="REMTREMBL:CAC86251"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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function="35S promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Cauliflower
'mol_type="other DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:83333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="other DNA"
strain="K12"
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97.9%;
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/gene="kan"
1075. .1869
/gene="kan"
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                                  2 (bases 1 to 6063)
Waterhouse, P.M.
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Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, ps., Singh, S.R., Abbott, D., Stoutiesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene silencing in plants
Plant J. 27 (6), 581-590 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          circular SYN 09-JUL-2002
             1245 TAATTATTTTCTTTTTCCTTTTAGTATAATAGTTAAGTGATGTTAATTAGTATGATT 4304
                                                                           4305 ATAATAATAGTIGITTATAATIGIGAAAAAATAATTATATAAAATAATATGITTACATAAA
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                                                                                                                                                                                                           1665 AGAGTAAGTATATTTTTTAATGAATTTGATCGAACATGTAAGATGATATACTAGCATT
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                                                     <u>ATAATAATATAGTTGTTATAATTGTGAAAAAAATAATTTATAAATATATATTGTTTACATAAA</u>
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Cloning vector pKANNIBAL
Cloning vector pKANNIBAL
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IBLDLMSGKLIESFRPEERFPMSTFKVLLCGAVLSRIDAGGEQLGGRIHVSQNDLVE
YSVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGFRELTAFLHNMGDHVTRL
DRWEPELNEAIFDNGSTTTMPAATTIRKLITGELLTASRQQLIDWMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKFSRIVVIYTTGSQATWDERNRQIA
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which was a derivative of pGEM-92f(-)"
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                                                                                       2 (bases 1 to 5824)
Waterhouse P.M.
Direct Submission
Submitted (G-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
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(protein id="Ca668250.1"
Darnef="G1:15982215"
(db_xref="G1:1598215")
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|Organism="Agrobacterium tumefaciens"
|mml_type="other DNA"
|db_xref="taxon:358"
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/mol_type="orther DNA"
/db_xref="taxon:167047"
/lab_host="Bscherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                organism="Escherichia coli K12"
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"mol_type="other DNA"
(db_xref="taxon:4227"
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/function="358 promoter"
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'strain="K12"
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/note="octopine
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/gene="pdk"
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Best Local Similarity 97.9%;
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/gene="amp"
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'gene="pdk"
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'gene="amp"
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094 09CACACTGGCCATATCGGTGGTCATCATGGCCAGCTTTCATCCCCGATATGCACCCCC 3785 097 731 09CACACTGGCGAGACTTTATCTGACAGCAGCCTGCCCCGGGAGGCATCACC 790 087 09CATAAAGTTCACGGGAGACTTTATCTGCACACGCACCTGCCCAGGGGGATCACC 790 087 09CATAAAGTTCACGGGAGACTTTATCTCACACACACACACA	BD2633 Compoi nucle BD2633 BD2633 BD2633 BD2633 Synth Synth Synth Artif Compo Compo Nucle Paten INVIT PR PR PR PR PR PR PR PR PR PR PR PR PR	CC pDONR206 CC May be any nucleotide CC May be any nucleotide CC May be any nucleotide CC May be any nucleotide FH Key FT misc_feature (1002). (1102) FT misc_feature (10080). FT misc_feature (10080). Location/Qualifiers Source 1. 5156 / organism="synthetic construct" / mol_type="genomic DNA" / M

PC PC

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DN Artificial Sequence

NN Artificial Sequence

PN JP 2002537790-4/156

PD J2.NOV-2002

PP 02-MAR-2000 JP 2000602252

PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAR-1999 US 60/136744

PI JAMES L HARTLEY,MCHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/ PC
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/db_xref="taxon:32630"
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Location/Qualifiers
BD263378.1 GI:33073146
JP 2002537790-A/156.
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                                                                                                                                                                                                                                                                                                                                          TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGGCCTTCCAAATGTTCTTCTCAA 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCCGATAACGGAGACCGGCACACTGGCCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGG
                                                                                                                                                                                             3318 AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACACATATCCAGTC
                                                                                                                                                                                                                                               GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATTT
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RESULT 7 BD263378/c LOCUS DEFINITION

ACCESSION

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GGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACC 730

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ALD Patent: JP 2002537790-A 157 12-NOV-2002;

NUTINGORN CORP

OS Artificial Sequence

BN JP 2002537790-A/157

OS Artificial Sequence

PN 12-NOV-2002

PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR

28-MAY-1999 US 60/122389,23-MAR-1999 US 60/126049 PR

28-MAY-1999 US 60/123744

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CC 12N15/09, CO7K14/00, C12N1/15, C12N1/19, C12N1/21, C12N15/PP

CC 212N15/09

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3144 CIGICACIGIAAIACGCIGCIICAIAGCACACCICTITITGACAIACTICGGGIAIACAI 3203
                                 3206 GATAACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTC 3265
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                                                                2904 GATAACGGCTCTCTCTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTC
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synthetic construct
artificial sequences.
1 (bases 1 to 4208).
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning of
                                                                                                                                       TOGICAGCAAAAGAGCCGTICATITCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGA
                                                                                                                                                                                                                                            TITICCGCTTTCCAGGGTTCGGCACGCAGGACGACGGCTTCATTCTGCATGGTTGTGCTT
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Pred. No. 6.5e-127;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                        Artificial Sequence
PN JF 2002537790-A/158
PN 12-0002537790-DA/158
PP 12-000 JP 2000602252
PF 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
PR 02-MAR-1999 US 60/136744
PI JAMBS L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC C12N15/09,CO7K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/ PC 00,C12N5/00
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                                                                                                                                                                                                                                                                                                                                                       feature (1326). (1326).
Location/Qualifiers
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Patent: JP 2002537790-A 158 12-NOV-2002;
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                                                                                                                   ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAGAACAATTTCACAAC 5064
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Synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 4165)
Harley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning of nucleic acids
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                 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAAATAAAAAACATCTACCT
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                                                                         1046 ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC 1105
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INVITROGEN CORP

ON Artificial Sequence

PN JP 2002537790-A/180

PD 12-NOV-2002

PP 02-MAR-2000 JP 2006602252

PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/135744

PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07X14/00,C12N1/15,C12N1/19,C12N1/21,C12N15/10,C12N15/PC
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986 ACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGGAGATATTGACATC
                       4596 ACGCAGACGACGACCTTCATTCTGCATGCTTGTGCTTACCAGACCGGAGATATTGACATC
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JP 2002537790-A/180.
synthetic construct
artificial sequences.
1 (bases I to 5584)
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning
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Pred. No. 4.4e-150;
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/organism='Artificial Sequence'
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Hartley, J., Drasch, M.A., Temple, G.F. and Cheo, D. Compositions and methods for use in recombinational cloning
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Length 4939;
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23.7%; Score 1108.8; DB 6 99.8%; Pred. No. 4.5e-150; iive 0; Mismatches 2;
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INVITROGEN CORP
OS Artificial Sequence
PN JP 200537790-A/155
PD 12-NOV-2002
PF 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/126049 PR 02-MAR-
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Compositions and methods for use in recombinational cloning of
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synthetic construct
artificial sequences.
1 (bases 1 to 4470)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning
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2224 ACRTHGGAFTGATTGGGAAGCTGGGTTCGAATTGGATAAGCTGGGTTAAGCTTGGGTAAGCTTGGGTAAGCTTGGGAAGCTGGGTAGGTTGGGGAAATTGGGTTGGGAAATTGGGTTGGGGAAATTGGGTTGGGGAAATTGGGTTGGGGTAAGCTTGGGTAAGCTTGGGAAATTGGGTAAGGTTGGAAAATTGGGTAAGGTTGGAAAATGGGGTAAGGAAATGGAAAAGGAAAATGGAAAATGGAAAATGGAAAATGGAAAAGGAAAATGGAAAAAGGAAAAAGGAAAAAA	du ç	17208 AACCG
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/translation="WREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREAVITREA
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LVDQDDLDEEHQGLAPAELFARLKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDC
GRLGVADRYQDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
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/note="octopine esynthase (ocs) terminator"
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/function="35S promoter"
14660. .16258
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/db_xref="GI:15982220"
                                                               1443. .2148
/note="NOS terminator"
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/note="left border"
7793. .9388
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Best Local Similarity 78.5%;
Matches 4460; Conservative
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          Gleave,A.P., Green,A.G. and Waterhouse,P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
21461301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="pHELLSGATE is a derivative of cloning vector
pART27"
                                                                                                                                                                                                                           Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
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264. .447
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function="NOS promoter"
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17922. .18691
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Cloning	BD263377 Compositi	composit	1 sodwon	Composit	Composit	Composit	BD263382 Compositi	A.7311872 Cloning v	V Duinoly 873 Laria	TE POST NOT DO THE	DELIGITE MODELL	A/9090 F.CLimervik	AZ3998 Din4 eAptes	AF187951 ACTIVATIO	A24783 plasmid prs	AR074388 Sequence	A24782 plasmid pJD	AR074387 Sequence	AY310901 Binary ve	Y18556 Cloning vec	BD217610 Method an	ner	A18050 DNA for tra	penc	nenc	I49885 Sequence 1	ance		M35007 A.tumefacie	AR007512 Sequence	AR084078 Sequence	AX052541 Sequence	loning	X00493 Agrobacteri	E00404 Ti plasmid	tragm	quence	thod o	AF242881 Agrobacte	loning		978 Binary v	218787 Cloning	J414108 Binary	410			DNA circular SYN 09-JUL-2002			yein phosphotransferase II; nptII		
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	DNA				eomycin p	tinomycin						n, N.A., w	.,D., stou	
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	CVE311874 18691 bp	Cloning vector pHELLSGATE.	AJ311874	AJ311874.1 GI:15982218	kanomycin resistance protein; neomycin phosphotransierase ii; mprii	gene; promoter; speC gene; spectinomycin resistance protein;	transposon Tn7.	Cloning vector PHELLSGATE	Cloning vector PHELLSGATE	artificial sequences; vectors.	-	Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Kouse, D., Alu, C.,	Gooding, ps., Singh, S.R., Abb	
RESULT I	CVESII8/4	DEFINITION	ACCESSION	VERSION	KEYWORDS			SOURCE	ORGANISM		REFERENCE	AUTHORS		

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, Ishii, K., Shiba, T. and Sakaki, Y.
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/ note="vector: pCR4.0TOP0; 10 million plasmodium yoelli
/ note="vector: pCR4.0TOP0; 10 million plasmodium yoelli
infected Anospheles stephens; mosquices and purified over
a DE52 cellulose column. The sporozoites were cultured for a DE52 cellulose column. The sporozoites were cultured for a DE52 cellulose column. Transformation of sporozoites into early excertibrocytic malaria parasites does not require host cells '(J Exp Med. (2003)197(08):1045-50). mRNA was cloned into a plasmid vector using Invitrogen's TOPO TA vector cloning kit."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 724)
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      New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 179
Email: bhanopol@med.nyu.edu
No Blast Hite ().
                                                                                                                                                                                 'organism="Plasmodium yoelii yoelii"
                                                                                                                                       Location/Qualifiers
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Pred. No. 1.2e-36;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
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CF469119 1037 bp mRNA linear EST 05-SEP-2003 P16A8 Plasmodium yoelli 17X axenic hepatic stages Plasmodium yoelii yoelii cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                            exoerythrocytic malaria parasites does not require host cells ' (J Exp Med. (2003)197(8):1045-50). mRNA was extracted using the Invitrogen microFAST TRACK kit and used for cDNA construction via the BDBiosciences SMART DNA synthesis kit. Double stranded cDNA was cloned into plasmid vector using Invitrogen's TOPO TA vector cloning kit."
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1 (bases 1 to 1037)
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Nung, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S., Nussenzweig, V. and Bhanot, P.
Expressed sequence tags from Plasmodium yoelii hepatic stages in
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Unpublished (2003)
Contact: Bhanot P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 845
                                                                                                                                                                 /organism="Ipomoea nil"
/mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/cultivar="Tokyo-kokei standard"
/clone="jml8n08"
/tissue type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"
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Medicine

Bow York University School of Medicine

So First Avenue, MSB 131, New York, NY 10016, USA

Tel: 212 263 5346

Tel: 212 263 8179

Email: bhanopol@med.nyu.edu

similar to NR [GI-23483806 hypothetical protein [Plasmodium yoelii)
yoelii] (e-108).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
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Unpublished (2003)
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Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.
Nussenzweig, V. and Bhanot, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                       Score 301.4; DB 12; Length 337; Pred. No. 4.8e-43; 0; Mismatches 1; Indels 1;
                     Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF469981.1 GI:34487353
         Contact: Tadasu Shin-i
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Best Local Similarity 99.4
Matches 313; Conservative
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Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Vaglio, P., Tzellas, N., Thierry-Mieg, D., Thierry-Mieg, J., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M. Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI174407 384 bp. mRNA linear EST 09-JUL-2001
OSTF043E11_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                              /db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
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Pred. No. 6.7e-50;
0; Mismatches 8; Indels 0;
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Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                       /organism="Caenorhabditis elegans"
/mol type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                             CDNAs were cloned into pPC86"
philippe_vaglio@dfci.harvard.edu
PoLYA=No.
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                                    Location/Qualifiers
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B1174407
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Note="The AD-wincoms."

RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
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1 (bases 1 Domoea.

Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
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44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Bmail: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans Ocloning project: Contact jerome_reboul@dfci.harvard.edu or
Pohlippe_vaglio@dfci.harvard.edu or
POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Caenorhabditis elegans"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGTGTTTTACAGTATTATGTAGTCTGTGTATTA
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida;
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.

1 (bases 1 to 384)
Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
Jackson,C., Shin-i,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
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Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project: Contact jerome_reboul@dfci.harvard.edu or
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/clone_lib="AD-wrmcDNA" library was generated with poly(A)+ /note="The AD-wrmcDNA library was generated with poly(A) RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 TIPATACGGCATTGAGGACAATAGCGAGTAGGCTGGATACGACGATTCCGTTTGAGAAGA 290
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                                                                                                                                                                                                     Length 487;
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Pred. No. 3.3e-51;
0; Mismatches 11;
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BII74407
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Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 539
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFcome cloning project : Contact david_hill@dfci.harvard.edu or
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OSTR151B2 1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
CB395230
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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
Armstrong, C.M., Li, S., Jacotch, L., Bertin, N., Janky, R., Moore, T.,
Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,
Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, W.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
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                                                                            TAPAATGATATAAATATCAATATATTAAATTAGATTTTGCATAAAAACAGACTACATAA 428
                                                                                                                                                                        427 TACTGTAAAACACAACATATCCAGTCACTATGAATCAACTTAGATGGTGTTTAGACGC
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                                                                                                                                                                                                                                                                                                                                                                             GACAGCCTTCCAAATGTTCTTCTAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGT
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/tissue_type="whole animal"
/dev_stage="mixed stage"
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/strain="N2"
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00 TCTCGTCAGAAAGGCCGTTCATTTAAAACTGCATTCACCAGTCCCTGT 430	RESULT 8 CB395230/c LOCUS LOCUS DEFINITION OSTRIS1B2 1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence. ACCESSION VERGION VERGION CB395230 VERGION KEYWORDS SOURCE Caenorhabditis elegans ORGANISM Caenorhabditis elegans ORGANISM ELWATYOLA; Metazoa; Nematoda; Chromadorea; Rhabditida;	REFERENCE 1 (bases 1 to 487) AUTHORS Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C. M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Jenna, S., Chevet, E., Papasotiropoulos, V., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P. P., Parcek, J., Papasotiropoulos, V., Doucette-Stamm, L., Hill, D.E. and Vidal, M.	expression JOURNAL Nat. Genet. (2003) In press COMMENT Contact: Vidal M Marc Vidal Laboratory Dana Farber Cancer Institute 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA Tel: 617 632 5739 Email: Marc Vidal@dfci.harvard.edu Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFecme	cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu	/db xref="taxon:639" /sex="Hermaphrodite and male" /tissue type="whole animal" /dev_stage="mixed stage" /done_lib="AD-wrmcDNA" /otone_lib="AD-wrmcDNA" /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the	Subsequent generation of CDNAs by Poly(A) pilling. The CDNAs were cloned into pPC86" ORIGIN Query Match Best Local Similarity 93.6%; Score 357; DB 14; Length 487; Matches 383; Conservative 0; Mismatches 25; Indels 1; Gaps 1;
QY 786 TCACCATCGGTGGCGGGGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGAT 945 Db 263 TCACCATCGGTGGCGGGGTGTCAATAATATCACTGTGTACATCCACAAACAGACGAT 322 QY 846 AACGGCTCTCTTTTTATAGGTGTAAACTGCATTTCACCAGTCCCTGTTCTCG 905 Db 323 AACGGCTCTCTTTTATAGGTGTAAACTGCATTTCACCAACCCCTGTTCTCG 905 Db 323 AACGGCTCTCTTTTTATAGGTGTAAACTGCGTTTTCACCAGCCATTCCCCTGTTCTCG 381 QY 906 TCAGCAAAAGAGCCGTTCATTCAATAAAACGGGGGACCTCAGCCATCCC-TTCCTGATT 964 Db 382 TCAGCAAAAGAGCCGTTCATTCAATAAAAACGGGCGACCTCAGCCATCCCTTTCCTGATT 441 QY 965 TTCCGCTTTCCAGCGTTCATTAATAAAAACGGGCGACCTCAGCCATCCCTTTCCTGATT 441 QY 965 TTCCGCTTTCCAGCGTTCCACAGACACACACACACACACA	RESULT 7 AGG00763/c AGG00763 722 bp DNA linear GSS 06-FEB-1999 LOCUS DEFINITION Homo sapiens genomic DNA, 21q region, clone: 64EllX4, genomic DEFINITION AGG00763. ACCESSION AGG00763.1 GI:2579571 KEYWORDS Homo sapiens (human) SOURCE Homo sapiens (human) CRGANISM Homo sapiens (human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 722) AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y. TITLE Homo sapiens genomic DNA, chromosome 21q JOURNAL Published Only in DataBase (1997) REFERENCE 2 (bases 1 to 722) AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y. TITLE Direct Submission JOURNAL Submitted (31-OCT-1997) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,	Sagamihara 228, Japan (B-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561) FEATURES 1. 722 722	Query Match Best Local Similarity 92.2%; Pred. No. 3e-60; Matches 495; Conservative 0; Mismatches 31; Indels 11; Gaps 7; Qy 601 GTTAATGGGTTTTTGGTGTTTTTCGGGTGAATCAGCCATTTTCCCCGAT 60 Db 722 GTTAAAGGCTTTTTGGANGAATTTCGGGTGGCTGAGATCGCCAATTNTTCCCGA 667	QY 661 AACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCCGAT 720 Db 666 TAAGGAGACCGGCACA-TGGCCATAACGGTGGTCATCA-GCGCCAGCTTTCA-CCCCCGAT 610 QY 721 ATGCACCACGGGTAAAGTTCACGGGAGCTTTATCTGACAGCAGGTGCACTGGCCAG 780 Db 609 ATGCACCACGGGTAAAGTTCACGGGAGCTTTATCTGACAGCAGCGTGCACTGGCCAG 550	Qy 781 GGGGATCACCATCCGTCGCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAAAA 840 Db \$49 GGGAATCACCATCGCTCGCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAG 490 Qy 841 ACGATAACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGT 900 Qy 1

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM391 row: column: 05
High quality sequence stor: 68
High quality sequence stor: 256.
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/clone="INAGE:30346484"
/clone="INAGE:30346484"
/tissue_lipe="pre-eclamptic placenta"
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/lone lib="NIH MGC 148"
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/note="organ: placenta; Vector: pBluescriptR; Site_l:
all-xhoi; Site_2: BamH; Library is oligo-dr primed and
directionally cloned using primer
5-TTTTTTTTTTTTTTTTTTTVA.3', Size-selected for average insert
S:-TTTTTTTTTTTTTTTTTTA and organized to ROT 5. This is a primary size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation).
Library constructed by W. Brownstein (NIMH/NIGRI,
National Institutes of Health). Note: this is a NIH_MGC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
II (bases 1 to 522)
MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished (1999)
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Pred. No. 3.5e-61;
0; Mismatches 15; Indels
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                                                                                                                                                                                                        mRNA
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                        522 bp
189 TTTTGACATACTTCGGGTA 170
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E 1 (Dases 1 to 725)

E 1 (Dases 1 to 725)

Hattori,M., Ishli,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

E 1 (Dases 1 to 725)

E 2 (Dases 1 to 725)

E 3 (Dases 1 to 725)

E 4 (Dases 1 to 725)

E 5 (Dases 1 to 725)

E 6 (Dases 1 to 725)

E 6 (Dases 1 to 725)

E 7 (Dases 1 to 725)

E 8 (Dases 1 to 725)

E 9 (Dases 1 to 725)

E 1 (Dases 2 to 725)

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sapiens genomic DNA, 21q region, clone: £32E9X13, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

SS 1 (bases 1 to 723)

RS Hattori, M.; Ishii, K.; Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNA, chromosome 21q

LD 2 (bases 1 to 723)

Ex 2 (bases 1 to 723)

By Hattori, M.; Ishii, K.; Shiba, T. and Sakaki, Y.

Direct Submission

LD Submitted (31-00T-1997) Masahira Hattori, Kitasato University,

Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,

Tel:0427-78-932, Fax:0427-78-9561)
                                GSS 06-FEB-1999
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                                                 clone: 64E11X4, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.2%; Score 411.8; DB 25;
98.1%; Pred. No. 1.3e-62;
live 0; Mismatches 8;
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                                723 bp DNP
21g region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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                                                 Homo sapiens genomic DNA, survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="21"
/map="21q"
/clone="64E11X4"
                                                                                                         AG000761.1 GI:2579569
                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                              Homo sapiens
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Best Local Similarity
Matches 416; Conserv
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AG013450/c
LOCUS
                                                                                                       VERSION
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SOURCE
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RESULT 4
AG000761/c
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           Tissue Procurement: Dr. Stefan Hansson

CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carnino: Michael J. Brownstein (LINI)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINI at:

http://image.llnl.gov

Plate: NDAM387 row: c column: 24

High quality sequence start: 144

High quality sequence stop: 251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 CCACCGGGTAAAGTTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 AACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGCCCCTGTTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.8%; Score 437.2; DB 14; Length 542; 95.5%; Pred. No. 4.8e-67; cive 0; Mismatches 18; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCAGACCGG-AGATATTGACATCATATATGCCTT 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCAGACCGGAAGATATTGACATCATATATGCCCT
                                                                                                                                                                                                                                     1. .542
/organism="Homo sapiens"
Smail: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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1 (Dases 1 to 542)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                         TATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTTTCGCGGGGGCTGAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGACGIGCACIGGCCAGGGGGATCACCAICCGICGCCCGGGCGIGICAAIAAIAICACT
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                                                                                                                                                                                     Length 713;
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AGENCOURT 13988518 NIH MGC 147 Homo sapiens CDNA clone IMAGE:30346919 5', mRNA sequence.
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                           643 AGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATATCGG
                                                                                                                                                                                         DB 29;
                                                                                                                                                                                       11.1%; Score 496.6; DB 2 94.2%; Pred. No. 1.5e-77;
                                                                                                                                                                                                                       0; Mismatches
Fax: 0427-78-9561)
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CD109790.1 GI:30753999
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Submitted (31-07-1997) Masahira Hattori, Kitasato University,
Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-cokyo.ac.jp,
                                                                                                                                                                          638
                                                                                                                                                                                                                                            698
                                                                                                                                                                                                                                                                                                                                                                                                              272
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Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Published only in DataBase (1997)
(bases I to 713)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
                                                                                                                                                                                                                                                                            94 GATCAGCCACTICTICCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCA 153
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Pred. No. 2.2e-81;
0; Mismatches 2; Indels 4;
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/clone="f65H12X16"
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                                                                                                                            Similarity 98.9
3; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasses 1 to 698)
E Hattori,M.; Ishii,K.; Toyoda,A.; Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Dublished Only in DataBase (1998)
E theses 1 to 698)
E Hattori,M.; Ishii,K.; Toyoda,A.; Shiba,T. and Sakaki,Y.
Direct Submission
L Department of Science, JST Sequencing Laboratory; Kitasato University, Dapartment of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@Agc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG012840 698 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: £65H12X16, genomic
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P1587 Pla
P1587 Pla
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12283V63
P13A3 Pla
P1-B8 Pla
P7-G5 Pla
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P7-G5 Pla
P1-B1 Pla
P13E12 Pl
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       CB997937 | CB997937 | CB997937 | CB395230 | CB395230 | CB395230 | CB4699119 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46994 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46993 | CF46933 
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	6 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA 32 	326 agaataagaaaagaggcctctttttggggaaaataaaagaaact ctact 385 	TCAAGAACAATTTCACAAC 44 TCAAGAACAATTTCACAAC 50	446 TCTIATACTITICTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 505	506 CTAAAGGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAACTGGCTGTGTATA 565 	566 AGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 625	626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 685 [686 TCGGTGGTCATCATGCGCCCAGCTTTCATCCCCGATATGCACCACGGGTAAAGTTCACGG 74	746 GAGACTITATCTGACAGCAGAGGACTGGCCAGGGGGATCACCATCGCCCCGGGG 805	806 GIGICAATAATAICACTCIGIACAICCACAAACAGACGAIAACGGCTCTCTTTIATAG 865 	866 GIGTAAACCITAAACIGCALTICCACGGTCCCGGTCAGCAAAGAGGCGGTTCAT 925	926 TICAATAAACCGGGCGACCICAGCCATCCCTTCCTGAITTTCCGCTTTCCAGCGTTCGGC 985	986 ACGCAGACGACGGCTTCATTCTGCATGGTTGTTGACAGACGGGAGATATTGACATC 1045	1046 ATATATGCCTTGAGCAACTGATAGCTGTCACTGTCAACTGTCATGTAATACGCTGCTTC 1105	1106 ATAGCACACCTTTTTGACATACTTCGGGTA 1137 	arch completed: May 10, 2004, 00:05:56 b time : 1230.96 secs
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	QY 806 GIGICAATAATATCACICIGIACAICCACAAACAGAGGATAACGGCICICICITITAIAG 865 Db 870 GIGICAATAAIAICACICIGIACAICCACAAACAGAGAIAACGGCICCICITITAIAG 929	QY 866 GTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAGAGCCGTTCAT 925	QY 926 TICAAIBAACCGGGGGACCICAGCCAICCCTTCCTGAITTTCCGCTITCCAGCGTTCGGC 985	OY 986 ACGCAGACGACGACGTCATTCTGCATGGTTACGAGACCGGAGATATTGACATC 1045	OY 1046 ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATAGGCTGCTTC 1105	OY 1106 ATAGCACACCTCTTTTGACATACTTCGGGTA 1137	RESULT 15 US-10-151-690-64	Sequence 64, Application US/10151690 Publication No. US20030124555Al GENERAL INFORMATION: APPLICANT: BRASCH, MICHAEL A.	£	; FILE REFERENCE: 0942.5120001 ; CURRENT APPLICATION NUMBER: US/10/151,690 ; CURRENT PILING DATE: 2002-05-21 ; DIRECT FILING DATE: TO-05-21 ; DIRECT FILING THE TO-05-21	FALCA EXPLICATION NOTIONS: 0. 10/131/030 PRIOR FILING DATE: 2002-05-21 PRIOR FILING DATE: 2001-05-21 PRIOR FILING DATE: 2001-05-21	NOTIFIED OF SEX ID NOS: 64 ; SOFTWARE: Patentin version 3.1 ; SEQ ID NO 64 ; LENGTH : 4627 ; TENGTH : 4627	· 🗷 🗗 🛛 -	Query M Best Lo	Caagitigtacaaaaagcigaacgagaacgiaaaatgatataaatatati 85 	QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTC 145

8 6 8 6 8 6 8 6 8 6	146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGAC	GENERAL INFORM APPLICANT: BR APPLICANT: BR APPLICANT: LAPPLICANT: LAPPLICANT: BR APPLICANT: BR APPLI	GENERAL INFORMATION: APPLICANT: CHEO, DAVID APPLICANT: CHEO, DAVID APPLICANT: CHEO, DAVID APPLICANT: LIX XIAO APPLICANT: ESPOSITO, DOMINIC APPLICANT: ESPOSITO, DOMINIC APPLICANT: ESPOSITO, DOMINIC APPLICANT: BYED, DEVON R.N. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC TITLE OF INVENTION OF TOWNER: US/10/151,690 CURRENT FILING DATE: 2002-05-21 CURRENT FILING DATE: 2001-05-21 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR PILING DATE: 2001-05-21 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR FILING DATE: 2001-05-21 NUMBER OF SEQ ID NOS: 64 SOFTWARE: Patentin version 3.1 SEQ ID NO 63 LENGTH: 4627 TYPE: DNA ORGANISM: Artificial sequence FEATURE: FRATURE: CHER INFORMATION: plasmid pDONR212 US-10-151-690-63
Sy Op	SO6 CTAAACGTCATAAAGTTICTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 565	Query Matc Best Local Matches 11	Query Match 24.7%; Score 1102.4; DB 15; Length 4627; Best Local Similarity 99.5%; Pred. No. 7.4e-157; Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY Dp	566 AGGGACCTGACATTIATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATT 625	Qy 2	26 GACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATACAATATTT 85
oy oy	626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 685	9 QY 8	86 AAATTAGAITTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTC 145
P võ	686 TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACGGGTAAAGTTCACGG 745	Qy 14	146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGAC
Q7.	746 GACACTITAICTGACAGCAGACGTGCACTGGCCAGGGGGAICACCAICCGICGCCCGGGC 805	Qy 20 Db 27	206 IGITCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA 265
oy Oy	806 GIGTCAATAATATCACTGTACATCCACAAACAGACGATAACGGCTCTCTTTTATAG 865 	Qy 26	266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA 325
Q <i>y</i>	866 GIGTAAACCITAAACIGCAITICACCAGICCCTGITCTCGICAGCAAAAGAGCGGITCAI 925 	Qy 32 Db 39	326 AGAAATAAGAAAAAGAGGTGGGAGCCTCTTTTTGTGTGACAAAATAAAACATCTACCT 385
vy Qu	926 ITCAAIDAACCGGGCGACCTCAGCCAICCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGC 985	Qy 38	386 ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC 445
% a	986 ACGCAGACGACGCTTCAITCTGCAIGGITGTGCTTACCAGACCGGAGAIATTGACATC 1045	QY 44	446 TCTIAIACTITICTCTIACAAGICGTICGGCTICAGGAITTITCAGCCTCTAIACTIA 505
ζς OP	1046 AINTAIGCCTTGAGCAACTGAIRACTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC 1105 [02y 50	506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCGGACTGGCTGTGTATA 565
oy Oy	1106 AFAGCACACCTCTTTTGACATACTTCGGGTA 1137 	2y 56	566 AGGGAGCCTGACATITAÎATICCCCAGAACAICAGGITAATGGCGITITITGATGTCAITI 625
RESULT 14 US-10-151 ; Sequenc ; Publice	14 151-690-63 ence 63, Application US/10151690 cation No. US20030124555Al	75 98 88 62 62 63 63 63 63 63 63 63 63 63 63 63 63 63	626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 685

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Sequence 62, Application US/10151690

| Sequence 62, Application US/10151690
| Publication No. US200301245581
| GENERAL INFORMATION:
| APPLICANT: BRASCH, MICHAEL A. |
| APPLICANT: CHEO, DAVID
| APPLICANT: LI, XIAO
| APPLICANT: ESPOSITO, DOMINIC
| APPLICANT: ESPOSITO, DOMINIC
| APPLICANT: BYRD, DEVON R.N. |
| TITLE OF INVERTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MC FILE REPRENCE: 0942.5120001
| CURRENT FILING DATE: 2002-05-21
| PRIOR APPLICATION NUMBER: US 10/151,690
| CURRENT FILING DATE: 2001-05-21
| PRIOR APPLICATION NUMBER: US 60/291,973
| PRIOR FILING DATE: 2001-05-21
| NUMBER OF SEQ ID NOS: 64
| SOFTWARE: PALENTIN VERSION 3.1
| SEQ ID NO 62
| LINGTH H.428
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US-10-151-690-62
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                                                          APPLICANT: CHEC, DAVID
APPLICANT: CHEC, DAVID
APPLICANT: LI, XIAO
APPLICANT: ESPOSITIO, DAVINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID N
FILE REPREBENCE: 0942-5120001
CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR PLILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 61
LENGTH: 5584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 4824
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99.8%; Pred. No. 8.6e-158;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; CTHER INFORMATION: plasmid pDONR207
US-10-151-690-61
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence
      Publication No. US20030124555A1
GENERAL INFORMATION:
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.9'
Best Local Similarity 99.8'
Matches 1110; Conservative
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                                                                                     ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGGCCGACAGCCTTCCAAA 281
                                                                   265
                                                                                                                         266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA 325
                                                                                                                                                 342 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA 401
                                                                                                                                                                               326 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTGTGTGACAAAATAAAAAACATCTACCT 385
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                                                                                                                                                                                             702 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACACTGGCCATA
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                                                                                                                                                                                                                                                                                                                CIAAACGIGAIAAAGIIIICIGIAAIIIICIACIGIAICGACCIGCAGACIGGCIGIGIAIA
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                                                                  TGTTCTTCGGGGTGATGCTGCCAACTTAGTCGACCGCCCTTCCAAATGTTCTTCTCAA
                                                                                                                                                                                                                                                                                                TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA
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US-10-151-690-61/c
; Sequence 61, Application US/10151690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACACAATATCCAGTC
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Pred. No. 8.2e-158;
0; Mismatches 2;
NAME/KEY: misc feature
LOCATION: (3327)..(563)
OTHER INFORMATION: attP1 recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (2513)..(2744)
OTHER INFORMATION: attP2 recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (3794)..(4537)
OTHER INFORMATION: pUC orlV / RK2 orlT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: gene
LOCATION: (959)...(1264)
OTHER INFORMATION: ccdB gene
FEATURE:
NAME/KEY: gene
LOCATION: (1606)...(2265)
OTHER INFORMATION: Cam(r) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.9%;
99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.8
Matches 1110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: gene
LOCATION: (2868)..(3677)
OTHER INFORMATION: Kan(r)
                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: terminator
LOCATION: (73)..(100)
OTHER INFORMATION: T2
FEATURE:
FEATURE:
COCATION: (232)..(275)
OTHER INFORMATION: T1
FEATURE:
NAME/KEY: terminator
LOCATION: (232)..(275)
OTHER INFORMATION: T1
COCATION: (232)..(275)
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US-10-357-268-1
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26 GACAAGTTTGTACAAAAAGGTGAACGGAAAGGTAAAATGATATAAATATCAATATTT 85 102 GCCAACTTTGTACAAAAAGGTGAACGAGAAAAGGTAAAATGATATAATATTTTTTGTACAAAAAAGGTGAAAAGGTAAAAAGGTAAAAAGGTAAAAAGGTAAAAAGGTAAAAAGGTAAAAAGGAAAAGGAAAAAGAAAAAA	26 ACGAMITCGCGGTATCCCCACTACCCCATCACCCCCATCCCAANGGTCTCCCAANGGTCTCCCCAANGGTCTCCCCAANGGTCTCCCCATCACCCCCAANGGTCTCCCCATCCCCAANGGCCTTCCCCAANGGTCTCCCCCCCCTCAATGCCCTTTTAAATCCTCAAAA 325 34 ACGAATCACCCCATCCCCCCCTCCCTCAATGCCCTCAATGCCCTTTAAATCATAAAA 325 402 ACAATAAAAAAAAAAAAAAAACCCCCCCCTCAATGCCCTCAAAAAAAA	06 ATAGCACP
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Oy 3509 AGGCTGTCGGTCGACTACAATACCATCTAAGTGTTGATTCATAGTGACTGG 3568	RESULT 10 Sequence 10.2 Application US/10151690 Sequence 10.2 Application US/10151690 Sequence 10.2 Application US/10151690 Sequence 10.2 Application US/10151690 SEQUENCE 10.2 APPLICANT: SECONOMIC USE 10.2 SEQUENCE 10.2 S	0

qa	13438 AAATIGITCTTGAIGCAGAIGATTTTCAGGACTAIGACACTAGCGTAIATGAATAGGIAG 13379	QQ	
85 SY	3329 AIGITITIAITITIGCACACAAAAAGGGCTGGCACCTCTITITTTTTTTTTT	δ Pp	321 TAAAAGAAATAAGAAAAAGAGGGGGGGGGGGCTCTTTTTGTGTGACAAAATAAAAACGTC 380
& a	3389 GATTTAATACGGCATTGAGGACAATAGCGAGTAGGCTGGATACGACGATTCCGTTTGAGA 3448 	\$ B	381 TACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTC 440
& 8	3449 AGAACATTIGGAAGGCIGICGGTCGACTAAGTIGGCAGCAICACCCGAAGAACATTIGGA 3508	Qy Dp	441 ACAACTCTTATACTTTTCTCTTACAAGTCGTTCGACTTCTTGGATTTTCAGCCTCTAT 500 16284 ATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGACA 16228
\$ A	3509 AGGCTGTCGGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTAGTGG 3568	oy Op	501 ACTIACIAAAGIGAIAAAGITICIGIAAITICIACIGIATGGACCIGGAGACIGGCIGG 560
QY Db	3569 ATAIGITGIGITITACAGIALTAIGIAGITCIGITITITTAIGCAAAAICIAATITAATAIA 3628 	λ O	561 GTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGT 620
<i>장</i> 유	3629 ITGATARITATARCHITITACGITICTGGITCAGCTITITIGIACAAACTIGICIAGAG 3687 	ò 8	621 CATITICGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGCACACTGG 680
RESULT US-10-	, 9 385-546-7/c	\dot{Q}	681 CCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCGGGGTAAGTT 740 16051ACTGGTGAAATGCAGTTTAAGGTTTACACCTATAAAAGAGAGAG
; Sequ ; Publ ; GENE	tence 7, Application US/10385546 ication No. US20030175783A1 RAL INFORMATION:	8 6	741 CACGGGAGACITIAICIGACAGCAGACGIGCACTGGCCAGGGGAICACCAICCGICGCC 800
APP APP APP	APPLICANT: Wesley, Susan; APPLICANT: Wesley, Susan; APPLICANT: Helliwell, Chris TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing	3 & 4	CGGGGGGGTGATCAATAATAATCACTCTGTACATCCACAACAGACGATAACGGCTCTCTTTTTTTT
CUR.	FILE REFERENCE: COLING OST. CURRENT APPLICATION NUMBER: US/10/385,546 CURRENT FILING DATE: 2003-03-12 PRIOR PEPLICATION NUMBER: US 60363852 PRIOR FILING DATE: 2003-03-14	Z ZZ	
0,	NUMBER OF SEQ ID NOS: 7 SOFTWARE: PatentIn version 3.0 LENG ID NO 7 LENGTH: 17476	Qy	915 GAGCCGTTCATTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTTTCCGCTTTC 974 15816 TCGGGGAAGAAGTGGCTGATCTCAGCCACCGGAAAATGACATCAAAAACGCCATTAACC 15757
	TYPE: DNA ORGANISM: Artificial PERTURE: OTHER INFORMATION: plasmid pHELLSGATE 8	yo da	975 CAGCGTTCGGCACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACCG 1031 15756 TGATGTTCTGGGGAATATAAATGTCAGGCTCCTTATACACAGCCAGTCTG 15706
US-10- Quer Best	-10-385-546-7 Query Match Best Local Similarity 62.4%; Pred. No. 4e-183; Length 17476;	Qy Db	1032 GAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCATCTG 1091 15705 CAGGTCGATACAGTAGAAATTACAGAAACTTTATCACGTTTAGTAAGTA
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3 8 8	141 CAGTCACTATGAATCAACTACTAGAATGGTATTAGTGACCTGTAGTCGACCGAC	\$ g	1208 TITAITTAITCTGCGAAGTGAICTTCCGTCACAGGTAITTAITCGGCGCAAAGTGCGTCG 1267
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g &	16524 CCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACAGCCTTCCAAATGTTCTT 16465 261 CTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCA 320	ð	1328 AGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAA 1387

1148 ACCITCALITICOCCAMACTICOCCAMACTICOCCACACCACACACACACACACACACACACACACACAC	2214 GATCTTACATTGGATTGATTACAGTTACCTTAGGCTTGGATCCTCTAGACC 2269	2270 ACTITGTACAAGAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATTAAAT 2329 	2330 TAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTCACTA 14385 TAGATTTTGCATAAAAACAGACTACATAATACTGTAAAAACACAACATATCCAGTCACTA	2390 TGAATCAACTACTTAGATGGTATTAGTGACTGTAGTCGACTAAGTTGGCAGCATCACCC 14325 TGAATCAACTAGATGGTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCC	2450 GACGCACTITGCGCCGAATAAATACTGTGACGGAAGATCACTTCGCAGAATAAATA	2510 CCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTT 2569	2570 GATCGGATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTT 2629	2630 TCAGCCTCTATACTTACTAAACGTCATAAAGTTTCTGTAATTTCTACTGTATCGACCTGC 2689 14089 AGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATGATGATGTCAATATCTCC 14030	2690 AGACIGGCTGTGTATAAGGGAGCTGACATTTATATTCCCCAGAACATCAG 2740 14029 GGTCTGGTAAGCACAAACGCAGAATGAAGCCGGTCGCCTCGCGTGCCGAACGCTGG 13973	2741 GITAAIGGGTITITGAIGTCAITITCGCGGTGGCTGAGAICAGCCACTICTTCCCCGAI 2800 13972 AAAGCGAAAAICAGGAAGGGTGGCTGAGCTCGCCCGGTITAITGAAAIGAAGGCTC 13913	2801 AACGGAGACCGGACACTGGCCATATCGGTGCTCATGCGCCAGCTTTCATCCCCGAT 2860 13912 TTTGCTGACGAGAACAGGGACTGGTGAATGCAGTTAAGGTTTAAGGTTAAGACCTATAA 13859	2861 AIGCACCGGGTAAAGTICACGGGAGACTTIAICTGACAGGAGGAGGGGGGG 2920 13858 AAGAGAGAGCGTIAICGTCTGTIGTGGATGIACAGACGTGATATTGACAGGCGG 13799	2921 GGGGATCACCATCCGTCGCCGGGCGTGTCAATAATATCACTCTGTACATCACAAACAG 2980	2981 ACGATAACGGTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGT 3034	3035 CCTGTTCTCGTCAGCAAAAGAGCCGTTCATTCAATAAACCGGGGGGACCTCAGCCATCC	b 13678 CAGTGEGGGTCTCCGTTATCGGGGAAGAAGTGGCTGATCTCAGCCACCGCGAAATGA 13619	y 3095 CTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGACGAGGCTTCATTCTGCA 3151	y 3152 TGGTTGTGCTTACCAGACGGAGATATTGACATCATATATGCCTTGAGCAACTGATA 3208	y 3209 GCTGTCGCTGTCACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA 3268	TAGAGGCTGAAAATCCAGATGAAGCCGAACGACTTGTAAGAGAAAAGTATAAAGATTGTG	Qy 3269 CTTCTGTTCTTGATGCAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAG 3328
	ACGTCTCATTTTCGCCAAAAGTTGGCCCAAGGCTTCCCGGTATCAACAGGGACACCAGGA 1207	THATTATTATTCGCGAAGTGATCTTCCGTCACAGGTATTATTCGCCGCAAAGTGCGTCG 1267 THATTATTATTCGCGAAGTGATCTTCCGTCACAGGTATTTATT	GGTGATGCTGCCAACTTAGTCGACTACAGTCACTATAGTAGTTGATTCAT 1327	AGTGACTGGAIAIGTGGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAA 1387 		GTCTCGAGGAATTCGGTACCAACTGTAAGGAAATAATTTTCTT 1493	GICTAGAGGATCCAAGCTTAICGATTTCGAACCCAGCTTCCCAACTGTAATCAATCAAA 15226 TITTCCTTTTAGTATAAAATAGTTAAGTGATGATAATTAGTATGATTATAATA	TGTTATAATTGTGAAAAATAATTATAAATATATTGTTTACATAAACAAAC	GACTAATTCATTTAATTAGTCAATCCATTTAGAAGTTAATAAAACTACAAGTATAT 15106 TAAAAAATATGACAAGTGATGTGTAAGACGAAGAAGATAAAAGTTGAGAGTAAGTA	15046	1793	AGCAG 14926 TATAA 1853	GTAIA 14866 TTAGA 1913	GATATTTAATTATAATAAATAATCAATAAAAAAATATTAATTTAATTTAATTTAATT 14806 AATTCCAATCTGCTTGTAATTATCAATAAACAAAATATTAAATAACAAGCTAAAGTAAC 1973	CTTATTTTACTATAGTATTTTATCATTAATTCATCAAACCAGCTAGAATTAC 14746	2033	2093	14626 2153	14566	TACTA 14506	

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15645 AATCCAGATGAAGCCGAACGACTTGTAAGAGAAAGTATAAGAGTTGTGAAATCCGATCA 15586
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CTCTAGACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAAT 16645
                                                                                           CATITICGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGG 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGCGTGTCAATATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTT
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Sequence 24, Application US/10055001A
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
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APPLICANT: Waterhouse, Peter
TITLE OF INVENTION: Using recombinational cloning
FILE REPERENCE: HELIGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
SUMMER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO SATER
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28.7%; Score 1277.8; DB 15
Best Local Similarity 62.4%; Pred. No. 4e-183;
Matches 2321; Conservative 0; Mismatches 1312;
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                                                                                                                                                             Length 17458,
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                                                                                                                                                          Score 1305; DB 15;
Pred. No. 3.1e-187;
0; Mismatches 1325;
                                                                                                           CTHER INFORMATION: acceptor vector pHELLSGATE11 US-10-055-001A-25
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NUMBER OF SEQ ID NOS: 26
SOFWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 17458
                                                                                                                                                                                           Matches 2308; Conservative
                                                                 TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                              Best Local Similarity
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Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
ITILE OF INVENTION: Using recombinational cloning
FILE REFERENCE: HELLGAR
FILE OF INVENTION: Using recombinational cloning
FILE PEPELCATION NUMBER: US/10/055,001A
CURRENT APPLICATION NUMBER: 2002-06-11
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US-10-055-001A-25/c
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                                               NAME/KEY: misc_feature
LOCATION: (16551)..(16319)
OTHER INFORMATION: attP2 recombination site (complement)
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (13675)..(13980)
OTHER INFORMATION: ccdB selection marker (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
LOCATION: (17610)..(16855)
OTHER INFORMATION: ccdB selection marker (complement)
                                                                                                                                                                                                         FEATURE:
MAME/KEY: misc_feature
LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (264)...(496)
OTHER INFORMATION: nopaline synthase gene promoter
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NAME/KEY: misc feature
LOCATION: (2149)..(2706)
COTHER INFORMATION: a left T-DNA border region
US-10-055-001A-13
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LOCATION: (13048)..(13279)
OTHER INFORMATION: attPl recombination site
PEATURE:
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LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination
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OTHER INFORMATION: nptII coding region
                                                                                                                                          NAME/KEY: misc feature
LOCATION: (14660)..(16258)
OTHER INFORMATION: pdk2 intron 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine
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LOCATION: (264)..(496)
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GENERAL INFORMATION:
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Using recombinational cloning
FILE REPRENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 18691
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                                                                                                                                            .7501 GACACCGAGGGGGGAACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCGGCGGGG 17560
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                                                                                                                                                                                          CGCATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGG
                         4038 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTAC
                                                                                                          NAME/KEY: misc_feature
LOCATION: (17850)...(17659)
OTHER INFORMATION: attPl recombination site (complement)
FEATURE:
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NAME/KY: misc feature
LOCATION: (10706). (11324)
OTHER INFORMATION: right T-DNA border fragment
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NAME/KEX:
NAME/KEX:
COCRION: (11674)..(13019)
OTHER INFORMATION: CaMV35S promoter fragment
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LOCATION: (7922)..(9985)
OTHER INFORMATION: spectinomycin resistance
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US-10-055-001A-13
; Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
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2719 ANTITUTE CONSTRUCTOR AND CONTITUDATION	16960 TTCAATTCTGTTGTGCACGTTGTAAAAACCTGAGCATGTGTGGCTCAGATCCTTACCGC 3798 CGGTTTCGGTTCATTCTAATGAATATATCACCCGTTACTATCGTATTTTTATGAATAATA 17020 CGGTTTCGGTTCATTCTAATGAATATATCACCCGTTACTATTTTATGAATAATAATA 3858 TTCTCCGTTCAATTTACTGATTGTACCCTACTATTTATGTACTAATTTAAAAATGAAA 17080 TTCTCCGTTCAATTTACTGATTGTACCCTACTATTATGTACAATATTAAAATGAAA 3918 CAATAATTATTACTGATTGTACCCTACTACTTATATGTACAATATAAAATGAAA 17140 CAATAATATTATTATTATAAAAATGCGACCACTATTAAAAAAAA	4038 17260 4098 . 17320 4158	17380 4218 17440	17500 GCAGCATTTTTTGGTGTATGGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGA 1338 CGACAAATCGTTGGGGGGTCCAGGGCGAATTTTGGGACAACATGTCGAGGCGCAGGGG 13560 CGACAAATCGTTGGGGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGGAGG 17560 CGACAAATCGTTGGGGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGG 1398 ACTTGCAAGCAAGCTAGCAAGCTTACTAGTGATGCATAGTATTTTATAGTATAGTGTCAGGCGCAAAATCT	17620 ACCTGCAGGCATGCAAGCTACTAGTGATGCATATTCTATAGTGTCACCTAAATCT 4458 GC 4459 17680 GC 17681	RESULT 5 US-10-055-001A-23 US-10-055-001A-23 ; Sequence 23, Application US/10055001A ; Publication No. US20030049835A1 ; APPLICANT: Wesley, Susan V. ; APPLICANT: Weterhouse, Peter	AFFLICANI: HELLIWELL, CULLECOPAGE A. TITLE OF INVENTION: Method and means for producing efficient silencing construct; TITLE OF INVENTION: Using recombinational cloning; FILE REFERENCE: HELLGA CURRENT APPLICATION NUMBER: US/10/055,001A CURRENT FILING DATE: 2002-06-11 NUMBER OF SEQ ID NOS: 26 ; SOFTWARE: Patentin version 3.1	; SEQ ID NO 23 ; LENGTH: 17862 ; TYPE: DNA ; ORGANISM: Artificial sequence ; FEATURE: ; OTHER INFORMATION: acceptor vector phELLSGATE4 US-10-055-001A-23
ANTICHETALITICACCIONACATCAGGITTITICACCIOTATIVACGGAGCCCCGA ANTICACACACACACACACACACACACACACACACACACACA	4 3 4 3 4 3 4 3 4 	8 8 8 8	46 66 6	3 8 8 8 	3 A & B	KD		
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US-10-055-001A-26

Sequence 26, Application US/10055001A

Publication No. US20030049835A1

GENERAL INFORMATION:

APPLICANT: Weeley, Susan V.

APPLICANT: Waterhouse, Peter.

APPLICANT: Waterhouse, Peter.

TITLE OF INVENTION: Method and means for producing efficiency of INVENTION: Method and means for producing in TITLE OF INVENTION: Using recombinational cloning;

FILE REFERENCE: HELLGA;

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT APPLICATION NUMBER: US/2001A

CURRENT PILING DATE: 2002-06-11

NUMBER OF SEQ 1D NOS: 26

SOFTWARE: PatentIn version 3.1

LENGTH: 17681
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US-10-055-001A-26
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Best Local Similarity 95.0%;
Matches 4449; Conservative
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                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial
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                                            APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Hillwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing critice of INVENTION: using recombinational cloning
TITLE OF INVENTION: using recombinational cloning
FILE REFERENCE: HELICAN
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 17476
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Pred. No. 0;
0; Mismatches
       Sequence 24, Application US/10055001A Publication No. US20030049835A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.4%;
Matches 4450; Conservative
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                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial
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US-10-055-001A-24
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11: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
                                                                                                                                              8, 2004, 10:39:35; Search time 1188.96 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-055-001A-24
US-10-355-546-7
US-10-055-001A-23
US-10-055-001A-13
US-10-055-001A-25
US-10-055-001A-25
US-10-055-001A-25
US-10-151-690-61
US-10-151-690-62
US-10-151-690-62
US-10-151-690-62
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4459
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                                                                                                                                                                                                                                                                                                                                                                                                                       2941586 seqs, 2264995651 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                nucleic search, using sw model
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Maximum DB seq length: 2000000000
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4,629	2	Sequence 5, Sequence 9, Sequence 20		9, 581 21	equence 1, equence 61 equence 62 equence 64 equence 11
90	US-10-644-335-3 US-10-556-088-55 US-10-356-088-55 US-10-356-088-48 US-10-358-464-31 US-10-358-464-31	US-10-027-880-5 US-10-176-884-9 US-10-177-478-20 US-10-055-001A-13	US-10-023-208-63 US-10-241-596-137 US-10-151-690-20 US-10-097-034A-37 US-10-389-120-2 US-10-389-120-1	US-10-666-778-9 US-09-887-576-581 US-10-162-214-4 US-10-151-690-21 US-10-357-569-1	20000
15 15 15 15 15	11221	1115	15 15 17 16 16		15 15 13
4627 17862 17681 786	2116 2873 2873 3034 3034 4947	7599 2867 2867 18691	1846 5558 6464 7278 9249 10463	12789 11180 528 4470	5584 4428 4627 4627 2877
24.7 24.2 1.4.1 2.7.1	16.5 16.5 16.5 16.5	15.9 15.8 13.8	13.4 13.4 13.4 13.4 13.4	13.3 10.7 10.7	0.00 0.00 L
1102.4 1079.4 1072.8 769	735.6 735.6 735.6 735 735	710.2 703 703 621.6	793 793 793 793 793 793	597 593.8 478.8 406.8	4 4 00 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
15 17 18 18	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	26 27 28 29	3 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5	6 8 8 8 4 6 8 8 6 0	4 4 4 4 4 1 2 6 4 8
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ALIGNMENTS

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Sequence 25, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susen V.
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
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US-10-055-001A-25
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Matches 4459; Conservative
US-10-055-001A-25
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                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 base pairs
LENGTH: 416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLIGY: both
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
CRIGINAL SOURCE:
INDIVIDUAL ISOLATE: ccdB gene of plasmid pKIL 19
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMA10.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEPAX: 714-760-9502
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITALAGGIGIAAACCITAAACIGCAIT 886
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                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 1...378
OTHER INFORMATION:
US-08-379-614-3
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403 TGTGTATAACGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                               Query Match 7.3%; Score 325.4; DB 3; Best Local Similarity 99.7%; Pred. No. 7.9e-59; Matches 326; Conservative 0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/09/225,152A
CURRENT FILING DATE: 1998-01-04
PRIOR APPLICATION NUMBER: 08/379614
PRIOR FILING DATE: 1995-07-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 858 TTTTATAGGTGTAAACCTTAAACTGCA 884
                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(378)
OTHER INFORMATION: ccdB gene of pKIL 18.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/BE93/00051
FILING DATE: 02-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270 CLASOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08379614
Patent No. 5910438
                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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Patent No. 6180407
GENERAL INFORMATION:
APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
FILE REFERENCE: VANMA10.001CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.3%; Score 325.4; DB 2, Best Local Similarity 99.7%; Pred. No. 7.9e-59; Matches 326; Conservative 0; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
                                                                                                                                                                                                    34,115
FP: VANMA10.001APC
                                                                FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/BE93/00051
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMAIO.0012
TELECOMMUNICATION INFORMATION:
TELEFHONE: 714-760-6044
TELEFAX: 714-760-9502
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: Coding Sequence
; LOCATION: 1...378
; OTHER INFORMATION:
US-08-379-614-2
                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic DNA
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: both
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US-09-225-152A-2/c
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                                                                                                                                                                                                 Length 15397;
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| Patent No. 5910438
| GENERAL INFORMATION:
| APPLICANT: Bernard, Philippe
| TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR NUMBER OF SEQUENCES: 6 CORRESPENDENCE ADDRESS:
| ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                              Score 566.4; DB 2;
Pred. No. 1.8e-108;
0; Mismatches 1;
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                                                                                                                                                                                            12.7%;
99.8%;
    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERASTICS: LENGTH: 15397 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Matches 567; Conservative
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MEDIUM TYPE: Diskett
                                                                                                                  linear
                                                                                                                                   MOLECULE TYPE: DNA
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US-08-379-614-2/c
                                                                                                             TOPOLOGY:
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US-08-673-768-1
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                                                                                 7230 CATICTAATGAATATATCACCCGTTACTATCGTATTTTTTATGAATAATATTCTCCGTTCA
                                                                                                                        ATTTACTGATTGTACCCTACTACTATATGTACAATATTAAAATGAAACAATATATTGT
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                                                                                                                                                                                                              Sequence 1, Application US/08673768

Patent No. 5952546

GENERAL INFORMATION:
APPLICANT: Bechrock, John R.
APPLICANT: Howie, William J.
APPLICANT: Howele, William J.
APPLICANT: Lee, Kathleen Y.
TILLE OF INVENTION: Delayed Ripening Tomato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/673,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
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REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 012176-005010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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FILING DATE: 27-JUN-1996
CLASSIFFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
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US-08-673-768-1/c
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                ATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAACC 12002
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                                                                   CGGTCCAGCACGGCCGGGTAACCGACTTGCTGCCCCGAGAATTATGCAGCATTTTTT
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APPLICANT: Bedirook, John R.
APPLICANT: Dunsmuir, Pamela
APPLICANT: Howie, William J.
APPLICANT: Howie, Kathleen Y.
APPLICANT: Lee, Kathleen Y.
TITLE OF INVENTION: Delayed Ripening Tomato Plants
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYETRM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,768
FILING DATE: 27.-UNN-1996
CLASSIFICATION: 800
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Pred. No. 1.8e-108;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
TTY: San Francisco
STATE: California
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APPLICATION NUMBER: US 60/000,721

PRILING DATE: 30-UNL-1995

ATTORING DATE: 30-UNL-1995

ATTORING DATE: 31-UNL-1995

ATTORING DATE: 31-UNL-1995

ATTORING DATE: 31-UNL-1995

TELEPHONE: (415) 576-0200

TELEPHONE: (415) 576-0300

INFORMATION FROM SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08673768 Patent No. 5952546
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Best Local Similarity 99.8%;
Matches 567; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15397 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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94111-3834
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MOLECULE TYPE:
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US-08-673-768-1
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                                   Patent No. 5428147

APPLICANT: BARKER, RICHARD F.;KEMP, JOHN D.
TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/91,538
FILING DATE: 13-4012-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 440,432
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 741,034
FILING DATE: 1991
APPLICATION NUMBER: 741,034
FILING DATE: 20-JAN-1988
APPLICATION NUMBER: 144,775
FILING DATE: 10-NOV-1991
APPLICATION NUMBER: 173,624
FILING DATE: 10-UNN-1991
APPLICATION NUMBER: 26-574
FILING DATE: 10-UNN-1991
APPLICATION NUMBER: 285,748
FILING DATE: 10-UNN-1991
APPLICATION NUMBER: 285,534
FILING DATE: 10-UNN-1991
APPLICATION NUMBER: 848,514
FILING DATE: 10-UNN-1991
APPLICATION NUMBER: 848,535
APPLICATION NUMBER: 848,733
FILING DATE: 01-APR-1966
APPLICATION NUMBER: 835,354
FILING DATE: 01-APR-1966
APPLICATION NUMBER: 835,354
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Best Local Similarity 100.
Matches 707; Conservative
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RESULT 10
5428147-1/c
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10490 TGGGCGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGGGCT
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                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Bacterial
                                                                                                                                                                                                                                SEQ ID NO 3
LENGTH: 14194
               RESULT 9
US-09-577-424-3
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Best Local S
Matches 711
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                                            CATHER INFORMATION: /label= neo
OTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of Th5"
PEATURE:
NAME/KEY:
LOCATION: 3257..4315
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY: -
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 cauliflower mosaic virus isolate CabbB-JI'
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                                                                                                                                                                                                                                                               LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.73
Matches 711; Conservative
OTHER INFORMATION:
FEATURE:
NAME/KEY: -
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Sequence 3, Application US/09577424
; Patent No. 6525245
; GENERAL INFORMATION:
; APPLICANT: RADOAGS, David M
TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED
; TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; FILE REPRENCE: UNL2990
; CURRENT APPLICATION NUMBER: US/09/577,424
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 15.9%; Score 709.8; DB 4; Local Similarity 99.7%; Pred. No. 2.5e-138; Les 711; Conservative 0; Mismatches 2;
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NAME/KRY: -
LOCATION: complement (397..751)
LOCATION: /label= 3'nos
OTHER INFORMATION: /label= 3' nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: /note= "1' regulatory sequence containing the
OTHER INFORMATION: /note= "1' regulatory sequence containing the
NTHER INFORMATION: /note= "1' regulatory sequence containing the
NTHER INFORMATION: T-DNA nopaline synthase gene"
NAME/KEY: -
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OTHER INFORMATION: /label= 3583
OTHER INFORMATION: /note= "3583 promoter sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: complement (1025..1607)
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /note= "promoter derived from the TA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: complement (752..1024)
OTHER INFORMATION: /labble barstar
OTHER INFORMATION: /note= "coding region of the barstar
OTHER INFORMATION: Bacillus amyloliquefaciens"
                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= pUC18
/note= "pUC18 derived sequence"
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NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
STREET: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US) US 07/899,072
FILING DATE: 12-UNN-1992
FILING DATE: 12-UNN-1992
FILING DATE: 12-UNN-1992
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTONEY, AGENT INFORMATION:
NAME: SVENBEON, LEGNARGER: 2121-102PCT
TELECOMUNICATION NUMBER: 30,330
REFERENCE, NUMBER: 30,330
REFERENCE, NUMBER: 2121-102PCT
TELECOMUNICATION INFORMATION:
TELECHONE: (703) 205-8050
TELECHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
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                                                                                                                                                                                  ZIP: 2046
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1..396
OTHER INFORMATION: ,
OTHER INFORMATION: ,
FEATURE:
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NAME/KEY: -
LOCATION: COT
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        LOCATION: 3257...4315
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           3689 CCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTTCAATTCTGT
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                                                                                                                                                                                                                                                                                                                     15.9%; Score 709.8; DB 1; Length 6555; 99.7%; Pred. No. 2e-138;
                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                         NAME/KEY: -

LOCATION: 4316..6555

COCHER INFORMATION: /label= puc18

OTHER INFORMATION: /note= "puc18 derived sequence"
US-08-351-413-2
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Patent No. 5977433
GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.77
Matches 711; Conservative
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NAME/KEY: - 1608..2440
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: complement
OTHER INFORMATION: /
OTHER INFORMATION: /
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LOCATION: 1..396
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2453 ATTTACTGATTGTACCCTACTTATATGTACAATATTAAAATGAAAAAAATGT
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                                                                                            Length 5399;
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; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Lemans, Mark
; APPLICANT: Lemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS: 3
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
                                                                                                                                 Indels
LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                          15.9%; Score 709.8; DB 3; 99.7%; Pred. No. 1.9e-138;
                                                                                                                               0; Mismatches
                                                                                            Query Match
Best Local Similarity 99.7<sup>3</sup>
Matches 711; Conservative
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US-08-351-413-2
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COCATION: 2101..3160
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note="13' regulatory sequence containing the OTHER INFORMATION: polyademylation site derived from the OTHER INFORMATION: polyademylation site derived from the OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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OTHER INFORMATION: /note= "35S3 promoter sequence derived from OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-JI" FEATURE:
GENERAL INFORMATION:

APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENITION: PROCESS FOR TRANSFORMING
TITLE OF INVENITION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
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LOCATION: 1285..2100
OTHER INFORMATION: /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycine OTHER INFORMATION: phosphotransferase gene"
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/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/084,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: CTABLE-PEUY, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
TELEPRONE: (703) 836-6620
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5399 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                               CITY: Alexandria STATE: Virginia COUNTRY: United States ZIP: 22313-1404 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: plasmid pDE108 FEATURE:
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NAME/KEY: - 452..1284
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LOCATION: 1..451
OTHER INFORMATION:
OTHER INFORMATION:
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TOPOLOGY: cir
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                                                                                                      FEATURE:
NAME/KEY:
LOCATION: 2101..3160
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note=""3' regulatory sequence containing the OTHER INFORMATION: plyadenplation site derived from the OTHER INFORMATION: polyadenplation site derived from the OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5399;
                           /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
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                                                                                                                                                                                                                                                                                                                                               LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.9%; Score 709.8; DB 3;
99.7%; Pred. No. 1.9e-138;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.73
Matches 711; Conservative
                                                                                                                                                                                                                                                                                                                            3161..5399
                           OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-475-975-1
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NAME/KEY:

RESULT 6 US-09-084-889-1 ; Sequence 1, Application US/09084889

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2873 IIGGIGIAIGIGGCCCCAAAIGAAGIGCAGGICAAACCIIGACAGIGACGACAAAICGI 2932
                                                                                                                               2933 TGGGCGGCCAGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGGGCT 2985
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OTHER INFORMATION: /note= "35S3 promoter sequence derived from OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-JI"FEATURE:
                                                                    4349 TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT
                                                                                                                                                                                                                                                                            Sequence 1, Application US/08475975
; Sequence 1, Application US/08475975
; Patent No. 6002070
; GENERAL INFORMATION:
    APPLICANT: D'HALLININ, Kathleen
    APPLICANT: D'HALLININ, Kathleen
    APPLICANT: D'HALLININ, MONOCOTYLEDONOUS PLANTS
    TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
    TORBESPONDENCES: 5
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Burns, Doane, Swecker & Mathis
    STREET: George Mason Bldg., Washington & Prince Sts.
    CITY: Alexandria
    STATE: Virginia
    STATE: Virginia
    STATE: Virginia
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/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/475,975
FILING DATE: 07-UW-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
FILING DATE: 24-MAY-1993
APPLICATION NUMBER: EP 9040332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REPERENCE/DOCKET NUMBER: 36,113
REPERENCE/DOCKET NUMBER: 36,113
REPERENCE/DOCKET NUMBER: 30,113
REP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-1404
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: plasmid pDE108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5399 base pairs
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STRANDEDNESS: double
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 49
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US-08-475-975-1
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LOCATION: 2101..3160
LOCATION: 2.01..3160
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
OTHER INFORMATION: site derived from the Agrobacterium T-DNA octopine synthase
OTHER INFORMATION: gene"
FEATURE:
                                                                                                                     NAME/KEY: -
LOCATION: 452..1284
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from Cauliflower mosai
OTHER INFORMATION: virus isolate Cabbb-JI"
                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: -
LOCATION: 1285..2100
OTHER INFORMATION: /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycine phosphotransferase gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4169 GATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGCCACCATTCAAC 4228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2813 ccestrocascacescescesceastracesacriscrescescasarrarecascarritr 2872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGGIGIAITGIGGGCCCCAAAIGAAGIGCAGGICAAACCIIGACAGIGACGACAAAICGI 4348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGAATAGGTTATAGCGACATCTATGATAGAGCGCCACAATAACAAATAGCGTTT 2572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTATTACAAATCCAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTAAAAGACTGAT 4048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTATTACAAATCCAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTAAAAGACTGAT 2632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTTACTGATTGTACCCTACTTATATGTACAATATTAAAATGAAAACAATATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3749 TGTGCACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                    /label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.7
Matches 711; Conservative
                        OTHER INFORMATION:
OTHER INFORMATION:
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4169 GATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAAC 4228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-UN-1955
CLASSIFICATION: 435
PRIOR APPLICATION 135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9040332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        %30-08-478-015-1

; Sequence 1, Application US/08478015

; Patent No. 5712135

; GENERAL INFORMATION:

APPLICANT: D'HALLUIN, Kathleen;

APPLICANT: GOBEL, Elke
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REGISTRATION NUMBER: 39,300
REPERENCE/DOCKET NUMBER: 010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: plasmid pDE108
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TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE
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OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note="1" regulatory sequence containing the OTHER INFORMATION: polyademylation site derived from the OTHER INFORMATION: polyademylation site derived from the OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
                                                                                                                                                                                                                                                                                                                                    /label= 35S3 /note= "35S3 promoter sequence derived from cauliflower mosaic virus isolate CabbB-JI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: -
LOCATION: 1285..2100
OTHER INFORMATION: /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycine OTHER INFORMATION: phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                                                                                                                                                   /label= pUC18
/note= "pUC18 derived sequence"
  TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 99.7%;
Matches 711; Conservative
                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pDE108
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                                                                                                                                                                                                                                                                                                                 452..1284
                                                                                                                                                                            NAME/KEY: -
LOCATION: 1..451
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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NAME/KEY:
                                                                                                                                                                         NAME/KEY:
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2753 GATICCTIGAAGTIGAGIATIGGCCGICCGCTCTACCGAAAGTIACGGGCACCATICAAC 2812
                                                                                                                                                                  4289 TIGGIGIAIGIGGGCCCCAAAIGAAGIGCAGGICAAACCIIGACAGIGACGACAAAICGI
                                                                                                                                                                                                     2873 TTGGTGTATGTGGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACCAGTGACGACAAATGCGT
                                                                                                        2813 ccediccaecacececececaraaccaacineciecececaaaaitaiecaecaiitii
                                                                                                                                                                                                                                                                                                          2933 TGGGCGGCTCCAGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGGCT
                                                                                                                                                                                                                                                                             4349 TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT
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STREET: P.O. DCC.
CITY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READBLE Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROME PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,015
FILING DATE: 07-UUN-1995
FILING PATE: 07-UUN-1995
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4099
                                    4136 AAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGA
                                                                                                                                                                                                                                          1256 CATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1040 AAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCCAGGGGCTAGTATCTACGA
                                                                                                 4100 CACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCCGGTTCCCCGCCGGCGCG
                                                                                                                              4196 CACACCGAGCGACGACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCCGCCGGCG
                                                                                                                                                                                                   CATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                      AGCATTTTTTTGGTGTATGTGGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACG
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                                                                                                                                                                                                                                                                                                    CCATTCAACCCGGTCCAGCACGCGGCCGGGTAACCGACTTGCTGCCCCGAGAATTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Burns, Dane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STAFE: Virginia COUNTRY: United States ZIN: 22131-1404 CONPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: RPLING DATE: 24-MAY-1993 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SINGUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-UUL-1991
ATTONNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08064121
Patent No. 5641664
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STRANDEDNESS: double
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US-08-064-121-1
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NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
NOCATION: 3666-1491
COCATION: 3666-1491
COTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: Containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                  gen
                                                                                                                                                                                                                                                                                                                                                         from Agrobacteriu
                                                                                                                                                                              LOCATION: 1..1869
OTHER INFORMATION: /note= "Coding region of a OTHER INFORMATION: truncated bt2 (crylab) gene, also designated as the bt884 oTHER INFORMATION: truncated bt2 (crylab) gene, also designated as the bt884 oTHER INFORMATION: 1877..210
OTHER INFORMATION: /note= "3' regulatory sequence OTHER INFORMATION: containing the polyadenylation site derived from Agrobacte OTHER INFORMATION: T-DNA gene 7."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3980 ATTGCGTTTTATTATTACAAATCCAATTTTAAAAAAAGCGGCAGAACCGGTCAAACCTAA 4039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5684. 6541
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
FRATURE:
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LOCATION: 3006..3665
OCTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "35S promoter sequence OTHER INFORMATION: derived from Cauliflower mosaic virus." FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
| NAME/KEY: misc feature
| LOCATION: 7155..7639
| OTHER INFORMATION: /note= "TR1' and TR2' promoter
| OTHER INFORMATION: derived from Agrobacterium T-DNA."
                                                                                                      ORGANISM: plasmid DNA designated as pJD884
                               TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: 2480..3005
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Matches 730; Conservative
                                                                                    ORIGINAL SOURCE:
                                                                                                                                                           NAME/KEY: CDS
          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   4171
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4052 AAGACTGATTACATAATCTTATTCAAATTTCAAAAGGCCCCCAGGGGCTAGTATCTACGA 4111
                                              4159
                                           CACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGGTTCCCCGGCGGCG
                                                                                     4112 CACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGGTTCCCCGCCGGCGCG
                                                                                                                                   4160 CAIGGGIGAGAIICCIIGAAGIIGAGIAIIGGCCGICCGCICIACCGAAAGIIACGGGCA
                                                                                                                                                                            1172 cardodránarriccridandrichárridactericedereteracennalization
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                                                                                                                                                                                                                                                                                                              4280 AGCATTITITIGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SOETHERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
APPLICANT: VAN AARSSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B: Burns, Doane, Swecker & Mathis
P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-0CT-1991
PRIOR APPLICATION NUMBER: GB 92400820.4
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     010830-049
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APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/08232016 Patent No. 5952547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
REFERENCE/DOCKET NUMBER: 0108
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORNELISSEN, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 76.39 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4400 CTGCAGGCATGC 4411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4412 CTGCAGGAATTC 4423
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STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: CORNELL
APPLICANT: SOETAER
APPLICANT: STAM, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22313-1404
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NAME/KEY: misc_feature
LOCATION: 3582..4407
COTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: 1793..2026
LOCATION: 1793..2026
LOCATION: A poste= "3' regulatory sequence
OTHER INFORMATION: Containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 7071..7566
CHER INFORMATION: /note= "TR1' and TR2 promoter
CTHER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with
CTHER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."
US-08-232-016-23
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                                                                                                   /note= "Coding region of a truncated modified bt2 (cryIAb) gene, also designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3800 GITTCGGTTCATTCTAATGAATATATCACCCGTTACTATCGTATTTTTATGAATAATAT 3859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CICCGIICAAITIACIGAIIGIACCCIACIACITAIAIGIACAAIAITAAAAIGAAAACA 3931
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LOCATION: 5600..6457
LOCATION: 5500..6457
OTHER INFORMATION: /note= "Sequence complementary to
the No. 595247
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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chloramphenicol acetyl transferase gene."
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                                                                                                                                                                                                                                                                                                                              NAME/KRY: misc feature
LOCATION: 2396.2921
COTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
FEATURE:
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Pred. No. 2.3e-142;
0; Mismatches 2;
                    plasmid DNA designated as pPS0212
                                                                                                                                                          crylAb6 gene.
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ilarity 99.7%;
Conservative
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LOCATION: 2922..3581
OTHER INFORMATION: /not
OTHER INFORMATION: chlo
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NAME/KEY: misc_feature
TocamION: 7071..7566
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OTHER INFORMATION: 0
OTHER INFORMATION: 0
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Best Local Similarity
                                                                       CDS
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                           ORGANISM:
                                                                  NAME/KEY:
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TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                       Patent No. 5952547
GENERAL INFORMATION:
COUNTRY:
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-232-016-22
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US-08-478-015-1
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US-08-478-13-2
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US-07-590-988A-1
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Maximum Match 100%
Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
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APPLICANT: STAM, Maike
APPLICANT: DOCKK, Jan
APPLICANT: DOCKK, Jan
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
TUTHE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22313-140*

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
PTI.ING DATE: 03-NOV-1994
US-09-489-039A-4117

US-08-929-967-4

US-08-929-967-5

US-08-916-3

US-08-914-916-3

US-08-914-916-3

US-08-914-977-3

US-08-927-967-6

US-09-272-169-5

US-09-967-6

US-08-929-967-4

US-08-929-967-4

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CITY: Alexandria
STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                               US-08-929-967-6
US-09-027-169-5
                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: P39,300
REPERENCE/DOCKET NUMBER: 01083(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/08232016 Patent No. 5952547
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STRANDEDNESS: double
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Search completed: May 7, 2004, 18:29:07 Job time : 1060.16 secs

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                                                                                                           TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA
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                 ATAGCACACCTCTTTTGACATACTTCGGGTA 1137
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Pred. No. 8.9e-148;
0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                   insertion; recombination; nucleic acid selection; isolation; ds.
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                                                                            Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0
                                                                                                         Score 1102.4; DB 7
Pred. No. 8.9e-148;
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid for a second population, (c) mixing the second population of nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to recombine with some or all of the second target nucleic acid molecules to selecting and isolating nucleic acid molecules. The method is useful for selecting and isolating puncleic acid molecules. The present sequence represents the donor plasmid pDONR207 nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7; Length 5584;
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                                                                                                                                                                                                                                          Inserting a population of nucleic acids into a second target selecting and isolating nucleic acid molecules by mixing the population of nucleic acid with a second target nucleic acid.
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                                                                                                                                                                                     DRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 24.9%; Score 1108.8; DB 7; Best Local Similarity 99.8%; Pred. No. 1.1e-148; Matches 1110; Conservative 0; Mismatches 2;
                                                                                                                                                                                     Byrd
                                                                                                                                                                                     Esposito D,
                                                                                                                                                                                                                                                                                                   Disclosure, Fig 18B-C; 273pp; English
                                                                                                                         21-MAY-2001; 2001US-0291973P.
                                                                                           21-MAY-2002; 2002WO-US015947.
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                                                               28-NOV-2002
                                                                                                                                                                                    Brasch MA,
      Synthetic.
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recombination; nucleic acid selection; ds.
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nucleic acid isolation;
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encoding an attB1, attB2, attB1, attB2, attL1, attB2, attB1, attB2, attB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes isolated nucleic acid molecules (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
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   gene product targeting, fusion tag cleavage; ds
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99US-0126049P.
99US-0136744P.
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                                                                      Bacteriophage lambda
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Matches 1110; Conserv
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23-MAR-1999;
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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, and attB2 muclectide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination site sore region that enhances the efficiency of recombination between a first nucleic acid molecule comprising at recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the mutated att recombination site. (I), (III), (III), weetors and methods from the present invention are used for the recombinational cloning of att recombination are used for the recombinational cloning of antercents to intracellular locations, cleaving fusion tags from desired procteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicans, cloning into phages and cloning. (I), (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3696 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACAACATATCCAGTC 3755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL1, attL2, attR1 attL1 nucleotide sequence useful for the recombinational cloning of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 GACAAGTITGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATATT
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99US-0126049P.
99US-0136744P.
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                                                               Bacteriophage lambda
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23-MAR-1999;
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3695

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(first entry)

11-JAN-2001

AAC55525;

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1122 ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC 1181
                                                                                                                                                                                                                                                  gene fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moving an insert nucleic acid between vectors using site-specific recombination in vivo, useful for studying the biology of the organism, including array construction, reporter gene fusions, mutagenesis and protein production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises a method for moving an insert nucleic acid molecule between vectors, the method involves moving an insert nucleic acid from one vector to another using site-specific recombination. The method of the invention is useful for studying the biology of an organism, including array construction, reporter gene fusions, mutagenesis, protein production and characterisation. The present DNA sequence represents the plasmid vector pMK2010 of the invention.
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Pred. No. 1.1e-148;
0; Mismatches 2; Indels
                                                        ATAGCACACCTCTTTTGACATACTTCGGGTA
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                                                                                                                                                                                                                      Plasmid vector pMK2010 DNA sequence
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                                                                                                                                  ADA50329 standard; DNA; 4892
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Best Local Similarity 99.8%;
Matches 1110; Conservative
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comprising a second recombination site that interacts with the mutated att recombination site. (I), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of mucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking mucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning; (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the camplification of the present invention .. Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other; Indels DB 3; ; ; Score 1108.8; DB 3 Pred. No. 1.1e-148; 0; Mismatches 24.9%; Matches 1110; Conservative Best Local Similarity 98 146 222 282 462 582 102 162 206 266 342 326 386 446 522 999 642 746 908 Query Match 402 909 979 702 686 762 822 8 \times 9 Dp a d g Оp g ò ò ð δ g qq à ö δ Db à g g ò Ω ð ð ò à ò

2001US-0291973P. Li X, entry) (INVI-) INVITROGEN CORP. (first Cheo D, WPI; 2003-129436/12. WO200295055-A2. Nucleic acid nucleic acid 21-MAY-2001; 01-MAY-2003 28-NOV-2002. Brasch MA, Synthetic. 986 926 ABZ58767; RESULT 8 ABZ58767 g Ωþ 임 ò qq a ઠે à ò 161 145 221 205 281 265 341 325 401 385 461 445 521 505 581 565 625 685 745 805 865 641 701 761 881 941 821 85 AAATTAGATTTTGCATAAAAAAAAGAGTACATAATACTGTAAAACAGAACATATATCGAGTC TCGGTGGTCATCATGCGCCAGCTTTCATCCCCCGATATGCACCACCGGGTAAAGTTCACGG GCCAACTITGTACAAAAAGCTGAACGAGAACGTAAAATGATATAAATATATTT AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACATATCCAGTC ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA Acceartcercercercercerceraticercercartcerceration redederodericadareadericaterretecedaraaceaaaceacaeacaeara GAGACTTTATCTGACAGCAGCAGCACTGGCCAGGGGATCACCATCGGTCGCCCGGGC GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTTTATAG 26 GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATATT TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA refrictedesidariecreccaactrastreaceaceaceactreceaarerretreaea AGAAATAAGAAAAAGGGGGGGGCCTCTTTTTGTGTGACAAAATAAAAACATCTACCT ATTCATATACGCTAGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA CTARACGIGATAAAGITTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGG rcriaracirriciciracaagicaricagaricarciagariricagaciraracira AGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT Gaps 882

BP. ABZ58767 standard; DNA; 4470 Destination plasmid pDONR201 nucleotide sequence.

insertion; recombination; nucleic acid selection; isolation; ds.

21-MAY-2002; 2002WO-US015947.

Byrd DRN;

Esposito D,

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.

Disclosure, Fig 26B-C; 273pp; English.

The invention relates to inserting a population of mucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to crecombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence

Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

Query Match

Length 4470; DB 7; Score 1108.8; 24.9%;

Db 13378 ATGTTTTATTTGTCACACAAAAAAGGGCTCGCACCTCTTTTTCTTTTTTTT	CCS SUL		AX (LIFE-) LIFE TECHNOLOGIES INC. XX XX XX XX XX XX XX XX XX XX XX XX YT Isolated nucleic acid molecules encoding an attEl, attE2, attP1, attE2, PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the XX YX YX YX YX XX XX XX XX XX XX XX XX	The present invention describes isolated nucleic acid molecules (I) cucoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 cucleotide sequence. Also described are: (I) an isolated nucleic acid cuclecule (II) comprising one or more att recombination sites comprising cucle least one mutation in its core region that increases the specificity cucleotide sequence. Also described are: (I) an isolated second attless one mutation in its core recipied on a second attless one recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at cucleast one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the cucleast att recombination site and a second nucleic acid molecule
14445 ACTITGTACAAGAAAGGIGAAACGIAAATGATATAAATATAAATTAAAT	2630 TCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATGACCTGC 2689 14089 AGTGACAGTTGACAGCGACCTATCAGTTGCTCAATATGTTCTCTACTGTATGTCTC 14030 2690 AGACTGGCTGTGTATAAGGAGCCTGACATTTATATCCCCAGAACACTCC 14030 2691 AGACTGG	2861 ATGCACCACGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 2920 13858 AAGAGAGAGCGTTATCGTCTTTGTGGATGTACAGAGTGATATTATTGACACGCCGG 13799 2921 GGGGATCACCATCGTCGTCTGTTTGTGATAATATCACTCTGTACATCACAAACAG 2980 13798 GCGACGGATCACCACTCGCCGGGCGTGTCAATAATATCACTCTGTACATCCCCTGA 13739 2981 ACGATAACGGCTCTCTTTTATAGGTGTAAACCTTCAATCACCATTTCACCAGT 3034 13738 ACTTTACCGGTGGTAAACGGTGTAAACCTTAAACTGCATTTCACCAGT 3034	CCTGHTCGTCGGCAAAAGGCGTTCATTTCAATAACGGGGGGCCTCGGCGTCC 3094 CAGTGTGCCGGTTCTCTTCAATAACCGGGGGACTCCTGGCATCC 3094 CAGTGTGCCGGTTCTCGGGGAAAAAGTGGCTGATCTCAGCCCCCGGGAAAATGA 1361 CTTCCTGATTTTCCGCTTTCCAGCGTTCGGCAGCGAGACGAGGGGGCTTCTGCA 3151 CTTCCTGATTTTCCGCTTTCCAGCGTTCGGCAGCAGACGAGGGCTTCTGCA 3151 CTTCCTGATTTTCCGCTTTCCAGCGTTCGGCAGAGAATATAAATGTCAGGCTCCCTTATACA 3151 CTTCCTGATTTTCCGCTTTCCAGAATATTGACATATAAATGTCTTGAGCAACTGATAA 3208 TGGTTGTGCTTACCAGACGAGAATTGACATATAAAATGTCTTGAGCAACTGATAA 3208 CAGCCAACTCTGAGAACTATTAAAAATGTCATAAAAATGTCTTGAGCAACTGAAAAAAAA	GCTGTCGCTGTCACTGTAATACGCTGCTTCATAGCACCTCTTTTTGACATA 3268 TAGAGGCTGAAAATCCAGATGAACGCTGCTTGTAGGAAAATTTTTGACATA 3268 TAGAGGCTGAAAAATCCAGAATGAACGAACGACTGTGTAGGAAAATTAGGTTGTG 1343 CTTCTGTTCTTGATGCAGATGATTTTCAGGACTATGACACTAGCGTATATGATAGGTAG 3328 AAATTGTTCTTGATGCAGAATGATTTTCAGGACTATGACACTAGCGTATATGATAGGTAG 1337 AAATTGTTCTTGTCACAAAAAAAAAGGGCTCGCACCTTTTTTTT

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13120 TATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTTAATATATTGATATTTATATATCATTT 13061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13480 ATGAAGCCGAACGACTTGTAAGAGAAAGTATAAGATTGTGAAATTGTTCTTGATGCAG 13421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3113 TCCAGCGTTC---GGCACGCAGACGACGACTTCATTCTGCATGG---TTGTGCTTACCA 3166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3167 GACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGT 3226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3227 CACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCTGTTCTTGATGCAG 3286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4071 CAGCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAACC
                                                                                                                                                                                                                           .4011 ATGCAGAATGAAGCCCGTCGTCTGCGTGCC---GAACGCTGGAAAGCGGAAAATCAGGAA
                                                                                                                                                                                                                                                                                                        GTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2879 TTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3780 CCTGGCCAGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3053 AAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTTTCCGCTT
                                                                                                                                                  GTGTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2819 GGCCATATCGGTGGTCATCATGCGCCCAGCTTTCATCCCCCGATATGCACCACCGGGTAAAG
2648 AAACGIGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13060 TACGITICICGITICAGCITITITICIACAACTIGICICGAG 13020
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Sacherichia coll; (b) selectable marker region capable of being expressed in the recipient cell cand (c) a chimeric DNA construct comprising: (i) promoter or promoter cell or by prokaryotic RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerases, (ii) first, second, third and polyadenylation region functional in the eukaryotic cell. The first and polyadenylation stees, or the second and third recombination sites or the everyone cell. The first and recombination sites, or the second and third recombination sites, or the second and third recombination sites or the third and courth recombination sites, do not recombination sites, or the third and courth recombination sites, do not recombination sites, or the third and courth recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment the present invention can be used in a conventional breading scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16644 ATATTABATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ATATTAAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACAACATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16704 CTCTAGACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 CTCGAGACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acids. The present sequence represents an acceptor vector nucleotide
                                                                                                                                                                                      cloning; silencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.7%; Score 1277.8; DB 6; Length 17476; 62.4%; Pred. No. 1.1e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.1e-172;
0; Mismatches 1312; Indels
                                                                                                                                                                                      Chimeric nucleic acid construct, recombinational cl
recombination site; double stranded RNA; plant; ds.
                                                                                                                                               8 nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CSIR ) COMMONWEALTH SCI & IND RES ORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helliwell C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 74-83; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence from the present invention
                      BP.
ABQ82141/c
ID ABQ82141 standard; DNA; 17476
                                                                                                                                                                                                                                                                                                                                                                               24-JAN-2002; 2002WO-AU000073.
                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-0264067P.
2001US-0333743P.
                                                                                                                                                 Acceptor vector pHELLSGATE
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.3
Matches 2321; Conservative
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bscherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerases; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and courth recombination sites, or the second and third recombination sites, and second recombination sites, and preferably are identical. The first and second recombination site, and preferably are identical. The first and second recombination site, and preferably as same recombination sites, do not recombination site, and preferably courth recombination sites, do not recombine with each other or with a same recombination site, and a same recombination site, and second and the action of double-stranded RNA which can be used for silencing target nucleic and sequences. The vectors can also be used to convert a DNA fragment.

into an inverted repeat structure. Plants transformed with a vector the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of mucleic acids. The present sequence represents an acceptor vector nucleotide

Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;

from the present invention

sednence

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-

Claim 16; Page 83-93; 104pp; English

RNA

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Helliwell & IND RES

Waterhouse P,

Wesley S,

WPI; 2002-682669/73

SCI

(CSIR) COMMONWEALTH

Chimeric nucleic acid construct; recombinational cloning; silencing; Acceptor vector PHELLSGATE 11 nucleotide sequence SEQ ID NO:25. recombination site; double stranded RNA; plant; ds. DNA; 17458 (first entry) ABQ82142 standard; WO200259294-A1 11-DEC-2002 Synthetic ABQ82142; ABQ82142/(
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26-JAN-2001; 29-NOV-2001;

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16327 TACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAGAAGT 16267 1688 CTCTAGACAAGTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATATT 16627 1626 ATATTAAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAAACAGACATATC 16567 16507 16447 16387 200 140 260 320 441 ACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTAT 500 CTCAAACGGAATCGTCGTACTCCAGCCTACTCGCTATTGTCCTCAATGCCGGATTAAATCA CTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCA TACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTC 16566 CACTCACTATGAATCAACTACTAGATGGTATTAGTGACCTGTAGTGGCGGCGTT CCAAATGITCITCGGGTGATGCTGCCAACTTAGTCGACGGCCGACAGCCTTCCAAATGITCTT 16506 ccaaargricricgggrgargcrgccaacrragrcgacggcggccrgccaargricrr Length 17458; Pred. No. 1.5e-176; 0; Mismatches 1325; 29.3%; Score 1305; DB 6; 62.4%; Pred. No. 1.5e-176; Similarity 62.4%;)8; Conservative Best Local Simi Matches 2308; 81 261 381 201 21 16446 321 16326 141 Query Match d d a g à qq $\dot{\delta}$ 셤 δ 셤 ð à à

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The present invention describes a vector (1) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bscherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter; and (c) a chimeric DNA construct comprising: (i) promoter or promoter or egion capable of being recognized by RNA polymerases of a entaryotic cell or by prokaryotic RNA polymerases; (ii) first, second, third and fourth recombination sites; (iii) if the combination sites are capable of reacting with a same recombination sites, or the second and third recombination sites, or the second and third recombination sites, or the second and third recombination sites, or the second and third recombination sites, do not recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vectors is useful for producing large amounts of double-stranded RNA which can be used for silenting target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimneric gene for reduction of the phenotypic expression of nucleotide

sequence from the present invention

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-

Claim 13; Page 62-72; 104pp; English.

stranded RNA.

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Helliwell & IND RES

Waterhouse P,

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WPI; 2002-682669/73

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                                                                                                                                                                                                                                                                                                                                             Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 18691;
                                                                                                                                                                                                                                                                                                                                                                                   28; Indels 1137;
                                                                                                                                                                                                                                                                                                                                                               71.4%; Score 3182.2; 79.1%; Pred. No. 0; ive 0; Mismatches
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Best Local Similarity
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Chimeric nucleic acid construct, recombinational cloning, silencing, recombination site, double stranded RNA; plant; ds.

24-JAN-2002; 2002WO-AU000073. 26-JAN-2001; 2001US-0264067P. 29-NOV-2001; 2001US-0333743P.

WO200259294-A1 01-AUG-2002

Synthetic

Acceptor vector PHELLSGATE nucleotide sequence SEQ ID NO:13.

(first entry)

11-DEC-2002

AB082130

ВР

ABQ82130 standard; DNA; 18691

1917	2718 ATTITUDATECCOCOLOGICAL COCCUTATION CO	Db 16960 ††Chai†CrG††GrGCACGŤ†GTAAAAACCTGAGCATGTAGCTCAGATCCTTACCGC 17019
1859 ANTINGANIPATIANTITITITITITITITITITITITITITITITITIT	6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B	<u>a</u>
1859 ANTINGANIPATIANTITITITITITITITITITITITITITITITITIT		.
	ANTACCHARCETTACCARATTETETETETATACTACTACTACTACTACTACTACTACTACTACTACTA	2658 AAGITICUGTAATITCIACUGIATCGACCIGCAGAGGCUGTGIAAAGGAAGCULAAC 271 880 AAGITICUGIAATITCIACIGIAICGACCIGCAGACIGGCIGIGIAIAAGGGAGCCIGAC 159

region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and for fourth recombination sites; (iii) 3' transcription terminating and polyadenylation retgion functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination site, or the third and fourth recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing targer nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of mucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

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Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;

09 TTTCATTTGGAGAGGACACGCTCGAGACAAGTTTGTACAAAAAAGCTGAACGAGAAACGT Length 17681; Indels 10; DB 6; Score 4200; DB Pred. No. 0; 0; Mismatches 0; 94.2%; 95.0%; Conservative Similarity Best Local Sim Matches 4449; Н Query Match à

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420 rereacaaaaraaaacarcracrarrcararacecraererearaerecreaaaarca TGTGACAAAATAAAAACATCTACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCA 361 13360

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TCTGCATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCA TCTGGATTTTCAGCCTCTATACTACAACGTGATAAAGTTTCTGTAATTTCTACTGTA 421 481 TCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAG 541

661 AACGGAGACCGGCACACTGGCCATATCGGTGATCATGCGCCAGCTTTCATCCCCGAT GITAAIGGCGITITITGAIGICATITITCGCGGTGGCIGAGAICAGCCACTICITCCCCGAI 601

721 ATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCGAGACGTGCACTGGCCAG 780

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14679 14379 14619 14739 ATAATAGTAATTCTAGCTGGTTTGATGAATTAAATATCAATGATAAAATACTATAGTAAA 14799 14019 14079 14319 14439 14499 14559 1796 ATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG 13779 13899 AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTAGTG 14139 1200 14140 CCGARCAACGICTCAFTTTCGCCAAAAGTFGGCCCAGGGCTTCCCGGTAFCAACAGGGAC 14199 1380 1440 1556 1616 1736 1080 1140 1260 1320 096 TATAATTGTGAAAAATAATTTATAAATATATTGTTTACATAAACAACATAGTAATGTAA TTTTAATGAATTTGATCGAACATGTAAGATGATATACTAGCATTAATATTTGTTTTAATC ATAATAGTAATTCTAGCTGGTTTGATGAATTAAATATCAATGATAAAATACTATAGAAAA GGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCACAAAAAG CCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCCGGTATCAACAGGGAC **ACCAGGATITIATITATICIGCGAAGIGATCTTCCGTCACAGGTATITATICGGCGCAAAG** TGCGTCGGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTT 14260 TGCGTCGGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTT GALTCATAGTGACTGGATATGTTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTTATGCAA GATTCATAGTGACTGGATATGTTGTGTTTTTACAGTATTATGTAGTCTGTTTTTTTATGCAA **AATCTAATTTAATATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTA** AATCTAATTTAATATATTGATATTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTA CAAAGIGGICTCGAGGAATICGGTACCAAC----TGTAAGGAAATAATTATTTTTTT 14440 CAAAGIGGICICGAGGAATICGGIACCCCAGCIIGGIAAGGAAAIAAITAITITITT TATAATTGTGAAAAAATAATTTAAAATATATTGTTTACATAACAACATAGTAATGTAA Accaradocorcretrinaracorcraaacerraaacrecarricaceacrecerer GATITICCGCTTTCCAGCGTTCGGCACGCACGACGGCCTTCATTCTGCATGGTTGTGC TTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTC AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTAGTG GGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAG TCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGGGGCACCTCAGCCATCCCTTCCT retegreagedaaagegegreertrearaaagegegegegegegegegererreer ACGATAACGGCTCTCTCTT 1617 1441 1497 1557 1677 1081 1141 14320 1381 14380 14500 14560 14620 14680 1737 14740 1021 1201 1261 1321 841 13840 196 13720 781 13780 901 13900 13960 14020 14080

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Best Local Similarity 99.4%;
Matches 4450; Conservative
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                             CAGGGGCTAGTATCTACGACACACGGGGGGGAACTAATAACGTTCACTGAAGGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                               CTACCGAAAGTTACGGGCACCATTCAACCCGGTCCAGCACGGCGGCCGGGTAACCGACTT
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    CAGGGGCTAGTATCTACGACACACCGGGGGGGGAACTAATAACGTTCACTGAAGGGAACT
                                                                               CCGGTTCCCCGCCGCGCGCGCATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCGCT
                                                                                                                                                             CTACCGAAAGTTACGGGCACCATTCAACCCGGTCCAGCACGGCGGCCGGGTAACCGACTT
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29-NOV-2001; 2001US-0333743P.
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fourth recombination sites, (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and same recombination site, or the third and same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCATTTGGAGGAGGACACGCTCGAGACAAGTTTGTACAAAAAAGCTGAACGAGAAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.8%; Score 4406.6; 99.4%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence from the present invention
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1000 TATA-OGRIGAMACCTA-AMACCACATICCACTACTACACAAAAAACACCACACAAAAAACACCACAAAAACACCACA
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are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombination sites, or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide recombination sites, or the second and third recombination sites Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other; sequence from the present invention

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AACGGAGACCGGCACACGGCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCGGAT 13719 Ariecaccaccacagaranaacricacagagacrirrarcraacagacagagacaragacaa 13779 13359 TCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAG 13599 13240 ACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTC 13299 13419 13539 AAAATGATATAAATATCAATATTAAATTAGATTTTGCATAAAAAACAGACTACATAAT 13119 ACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC 13179 13239 TITCATITGGAGAGGACACGCTCGAGACAAGTITGTACAAAAAAGCTGAACGAGAAACGT 13059 540 720 ö 120 180 240 300 360 420 480 TCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCCAGAACATCAG 600 GITAATGGCGITITITGALGICALTITICGCGGTGGCTGAGATCAGCCACTICTTCCCCGAT 660 9 13480 TCTGGATTTTCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTA AACGGAGACCGGCACACTGCCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCCGAT ATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGCAGACGTGCACTGGCCAG reragricaccidacadeerrecaaarerrerregesrearerrecaacrragregaees ACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTC CTCAATGCCGTATTAAATCATAAAAAAAAATAAGAAAAAAGAGGGGGGGCCTCTTTTTG 13360 TGTGACAAAATAAAAACATCTACCTATTTCATATACGCTAGTGTCATAGTCCTGAAAATCA TCTGCATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCCTTCA TCTGGATTTTCAGCCTCTATACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTA AAAATGATATAAATATCAATATTAAATTAGATTTTGCATAAAAAACAGACTACATAAT TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG TGTGACAAAATAAAAACATCTACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCA TITCATITIGGAGAGGACACGCICGAGACAAGTITGTACAAAAAAGCTGAACGAGAAACGT ACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC Gaps Length 17458; ô Indels DB 6; ° 100.0%; Score 4459; 100.0%; Pred. No. 0; iive 0; Mismatches Best_Local Similarity 100. Matches 4459; Conservative 13660 541 601 199 721 13540 13600 13720 Н 13300 361 481 61 13060 13120 13180 241 301 421 13000 121 181

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	1 ACGATAACGGCTCTCTTTTATAGGTGTAAACCTTAAAACTGCATTTCACCAGTCCCTGT	cdataacddctctctttttataddtgtaaaccttaaactgcatttcaccactccctg	1 TCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCCACCTCAGCCATCCCTTCCT	GATTITICGGCTITCCAGGGTTCGGCACGCAGGGGCTTCATTCTGCATGGTTGTGC	ITTTCCGCTTTCCAGCGTTCGGCACGCAGGACGACGGCCTTCATTCTGCATGGTTGTG	1 TTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATGCTGTGTGCTGTGTCTTTTTTTT	CTGTCACTGTAATACGCTTGCTTCATAGCACACCTCT	TGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTAGT	1 CCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGGCTTCCCGGTATCAACAGGGACCCCGATCAACGTCTCCCGGTATCAACAGGGACCAAAAGTTGGCCAAAAAGTTGGCCAAAAAGTTGGCCAAAAAGTTGGCCAAAAAGTTGGCCAAAAAGTTGGCCAAAAAAGTTGGCCAAAAAAATTGGCCAAAAAAATTGGCCAAAAAAAA	ACCAGATTTATTTATTCGGAAGTGATCTTCCGTCACAGGTATTTATT	O ACCAGGATTATTATTCTGCGAAGTGATCTTCCGTCACGGGTATTTATT	1 TGCGTCGGGTGATGCTGCAACTTAGTCGACTACACGACTAATACCATCTAAGTAGTTGTT	0 IGCGICGGGGGGGCCCAACTIAGICGACTACAGGICACTAAIACCAICIAAGTAGI	1 GATTCATAGIGACIGGATAIGITGITITTACAGTATTAIGTAGTCIGTITITIAIGCAA	o darricaladridacidealardrididirirakararrarararararararararararararara	1 AATCTAATTTAATATTGATATTATATGATTTTAGGTTTCTGGTTCAGGTTTCTGTA	O ANA SECTION OF THE		1 TTTAGTATAAATAGTTAA	0 TITAGTATAAAATAGTTAAGTGATGATGATTAGTATGATTATAATA	1. ATTGTGAAAAATAATTTATAAATATATTGTTTACATAACAACALAGTAATGTAAAAAA	o attgrgaaaaataatttataaatatattgrttacataaacaacatagtaatg	11 ATATGACAAGTGATGTGAAAGACGAAGATAAAAGTTGAGAGTAAGTTATTTTTTTT	ANGARITIGATICARICARAGAIGATATACIAGAITATACATATATATATATATATATATATATATATATATA		-	O TAGTAATTCTAGCTGGTTTGATGAATTAAATATCAATGATAAAATACTATAGTAAAAAT)] AGAATAAATTAAAATAAATATTTTTTATAATAATAATTATT	O AGAATAAATTAAATTAAAATAATTTTTTTTTATGATTAATAGTTTATTA	1 TCTATACCATTACTAAATATTTTTAGTTTAAAAGTTAATAATATTTTGTTAGAAATTCCA
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ABQ82142 standard; DNA; 17458
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                                                      - nucleic search, using sw model
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	Description	Abq82142 Acceptor	Abq82141 Acceptor	Abg82143 Acceptor	Abq82130 Acceptor	Abq82142 Acceptor	Abq82141 Acceptor		Abz58767 Destinati	Ada50329 Plasmid v	Aac55525 Donor pla	Aac55632 Donor pla		Abz58768 Destinati	Abz58769 Destinati	Abz58770 Destinati	Abq82143 Acceptor	Aac55524 Donor pla	Aac55523 Donor pla	Aac55522 Donor pla	Aac55526 Donor pla	Aaz38603 Flaveria	Add44386 Flaveria	Aaq40419 Sequence
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AAQ42160	AAQ42159	AAZ60627	ACC85049	AAF25320	AAQ25706	AAQ53874	AAC66932	AAN50182	AAN50226	ABZ68391	ABQ82130	AAD44626	AAD27063	AAC55467	AAC55464	AAC55469	AAC55507	AAC55491	AAC55483	AAC55454	AAC55471	
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16.3	16.3	16.0	16.0	15.9	15.9	15.9	15.9	15.9	15.8	15.8	13.9	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	
728.8	728.8	713	711.4	710.2	709.8	709.8	709.8	707	703.8	703	621.6	597	597	597	597	597	597	597	597	597	597	
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ALIGNMENTS

BP.

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA. Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds. Acceptor vector pHELLSGATE 11 nucleotide sequence SEQ ID NO:25. (CSIR) COMMONWEALTH SCI & IND RES ORG. Helliwell C; 26-JAN-2001; 2001US-0264067P. 29-NOV-2001; 2001US-0333743P. 24-JAN-2002; 2002WO-AU000073. Waterhouse P, WPI; 2002-682669/73. WO200259294-A1. 01-AUG-2002. Wesley S,

SUMMARIES

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bacherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites, (iii) 3 transcription terminating and polymeration region functional in the eukaryotic cell. The first and

Claim 16; Page 83-93; 104pp; English.

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Db 4292 AGCATTTTTGGTGGGCCCCAAAGAGTGAAGCTTGACAGTGAG 4351

Oy 4340 ACAAATCGTTGGGGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGAG 4351

Db 4352 ACAAATCGTTGGGCGGGTCCAGGGCGAATTTTGCGACACATGTCGAGGTCAGGAG 4399

Oy 4400 CTGCAGGCATG 4411

Oy 4400 CTGCAGGCATG 4411

Db 4412 CTGCAGGAATT 4423

Search completed: May 9, 2004, 11:28:55

Job time: 11116.3 Becs
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4280 AGCATTTTTTGGTGTATGTGGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACG 4339
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8112 AAATCGTTGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT 8053
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Pred. No. 1.5e-95;

    . 7566
    Organism="synthetic construct"
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synthetic construct
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Best Local Similarity 99.7
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                                                                                                                                           complement (<8785. .>9420)
complement (8791. .9342)
/note="promotes resistance to glutamine synthetase"
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100.0%; Pred. No. 1.8e-96;
tive 0; Mismatches 0;
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/product="mannopine synthase"
/note="5' end and promoter"
                                                                        complement (8054. 8784)
/product="octopine synthase"
/note="3' end"
    /note="T-DNA right border"
7690. .7713
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/note="T-DNA left border"
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OY 2012 ACAAACATAATCTAATGCTAATATAACAAGCGCAAGATCTATTATATATA	RESULT 13 A23998 LOCUS LOCUS DEFINITION PIE4 expression vector. ACESSION A23998.1 G1:83338 KEYWORDS SOURCES OURGANISM SYNTHetic construct	artificial sequences. AUTHORS Nazarov, V., Botterman, J., Stanssens, P. and Sevcik, J. AUTHORS Nazarov, V., Botterman, J., Stanssens, P. and Sevcik, J. TITLE A novel ribonuclease and its inhibitor JOURNAL Patent: BP 0537399-A 3 21-APR-1993; PLANT GENETIC SYSTEMS, N.V FRATURES Location/Qualifiers 1. 7049 /mol_type="unassigned DNA" /db_xref="taxon:32630"	Query Match 16.8%; Score 747; DB 6; Length 7049; Best Local Similarity 94.6%; Pred. No. 3.7e-98; Matches 771; Conservative 0; Mismatches 44; Indels 0; Gaps 0;	OY 3604 TITATGCAAAAICTAATITAATATGATATTATATCATITTAGGTTCTGGTTCAGC 3663	3664		Qy 3784 CAGAICCTTACCGCGGTTTCGGTTCTAATGAATATATCACCGTTACTATCGTAT 3843	Oy 3844 ITITAIGAARATATICICCGTICAAUTIACTGATIGIACCCTACTACTTAITAIGIACAA 3903 bb 4242 ITITAIGAARAATATICICCGTICAATITACTGATIGIACCCTACTACTATAIGIACAA 4301	Qy 3904 TATTAAAATGAAAACAATATTGTGCTGAATAGGTTTATAGCGACATCTATGATGAGC 3963	OY 3964 GCCACAATAACAAACAATTGCGTTTTATTATTACAAATCCAATTTTAAAAAAAGGGGCAG 4023 DD 4362 GCCACAATAACAAACAATTGCGTTTTATTACAAATCCAATTTTAAAAAAAA	

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PR 08-APR-1999 US 09/056767,03-AUG-1998 US 09/127735 PI

PETER MICHAEL WATERHOUSE, MIN BO WANG, MICHAEL WAIN GRAHAM PC
C12N15/09, A0145/00, C12N15/10, C12N15/00, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N15/10, C12N
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                                                                                                                                                                   UF ACUASILED CONSTRUCT
SM synthetic Construct
synthetic Construct
artificial sequences.
E 1 (bases 1 to '986)
S Waterhouse, P.M., Wang, M.B. and Graham, M.W.
Method and means of obtaining improved phenotype
L Patent: UP 2002511258-A 7 16-APR-2002;
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
OS Artificial Sequence
PN JP 2002511258-A/7
PD 16-APR-1999 JP 2000543598
PR 07-APR-1999 US 09/056767,03-AUG-1998 US 09/127735 PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTACATAAACAACATAGTAATGTAAAAAAAATATGACAAGTGATGTGTAAGACGAAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 GTAAGGAAATAATTATTTTCTTTTTTCCTTTTAGTATAATAGTTAAGTGATGTTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 TTACATAAACAACATAGTAATGTAAAAAAATATGACAAGTGATGTGTAAGACGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAAAGTTGAGAGTAAGTATATTATTTTAATGAATTTGATCGAACATGTAAGATGATAT
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    786 bp DNA linear of obtaining improved phenotype.
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Pred. No. 3.6e-101;
0; Mismatches 0;
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                                                                                                                  BD194641.1 GI:33004386
JP 2002511258-A/7.
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L Submitted (03-MAY-1994) E. Rosche, Institut f. Entwicklungs- und Molekular-, biologie der Pflanzen, Heinrich-Heine-Universitaet, Universitaetsstr. 1, 40225 Duesseldorf, FRG
Location/Qualifiers
1. 14648

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F.trinervia pdk gene for pyruvate,orthophosphate dikinase.
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Rosche,E., Streubel,M. and Westhoff,P.
Primary structure of the photosynthetic pyruvate orthophosphate
dikinase of the C3 plant Flaveria pringlei and expression analysis
of pyruvate orthophosphate dikinase sequences in C3, C3-C4 and C4
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pdk gene; pytvavete,orthophosphate dikinase.
Flavoria trinervia
Flavoria trinervia
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Plant Mol. Biol. 26 (2), 763-769 (1994)
95036056
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EDTPFKDPRELYDFLKTEKPEEELVFSHGDLGDSNIFVKDGKVSGFIDLGRSGRADKW
YDIAFCVRSIREDIGEEQYVELFFDLLGIKPDWEKIKYYILLDELF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTCTGTTGTGCACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3681 TCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4493. .5234
/gene="pok"
/note="from pyruvate orthophosphate dikinase (pdk)"
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/note="octopine esynthase (ocs) terminator"
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                                                                                                                                                                                                                                                                                                                                                                             /organism="Agrobacterium tumefaciens"
|mol_type="other DNA"
|40 xref="taxon:358"
|1075. .1869
                                                                                                                                                 mosaic virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%; Score 779; DB 12; I
100.0%; Pred. No. 9.3e-103;
iive 0; Mismatches 0;
      K12"
                                                                                                                                                                                                                                                                organism="Flaveria trinervia"
      coli
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/function="358 promoter"
   /organism="Escherichia
/mol_type="other DNA"
/strain="K12"
                                                                                                                  104. .4449
organism="Cauliflower"
                                                                                                                                                                      /mol_type="other DNA"
/db_xref="taxon:10641"
                                                                                       'db_xref="taxon:83333"
                                                                                                                                                                                                                                                                                     /mol_type="other_DNA"
/db_xref="taxon:4227"
5288. .6053
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/gene="kan"
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/gene="pdk"
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Best Local Similarity 100.
Matches 779; Conservative
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Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, ps., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene silencing in plants
Plant J. 27 (6), 581-590 (2001)
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TCCGTTCAATTTACTGATTGTACCCTACTTATATGTACAATATTAAAATGAAAACAA 5279
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                                                                                                                                                                                                                                                                                     5460 ACACCGAGGGGGAACTAATAACGTTCACTGAAGGAACTCCGGTTCCCCGCCGGGGGC
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                                     TTGCGTTTTATTATTACAAATCCAATTTTAAAAAAAGCGGCAGAACCGGTCAAAACCTAAAA
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Cloning vector pKANNIBAL
Cloning vector pKANNIBAL
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2601, AUSTRALIA
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/organism="Cloning vector pKANNIBAL"
/mol type="other DNA"
/db xref="taxon:167048"
/lab host="Escherichia coli"
/focus
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Waterhouse, P.M.
Direct Submission
Submitsed (04-MAY-2001) Waterhouse P.M.,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT
Location/Qualifiers
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ACCESSION
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JOURNAL
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CVE311873
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                                                                                                                                                    /note="pHANNIBAL is a derivative of cloning vector pART7 which was a derivative of pGEM-92f(-)"
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     Canberra, ACT 2601, AUSTRALIA
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/note="octopine esynthase (ocs) terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /producT="ampicillin resistance protein"
/protein_id="CAC86250.1"
/db_xref="G1:15982215"
/db_xref="G1:15982215"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Agrobacterium tumefaciens"
|mol_type="other DNA"
|db_xref="taxon:358"
                                                                                                                                                                                                                                                                                                    'organism="Cauliflower mosaic virus"
                                                        /organism="Cloning vector pHANNIBAL"
/mol type="cother DNA"
/db xref="taxon:167047"
/lab_host="Escherichia coli"
                                                                                                                                                                                                            K124
                                                                                                                                                                                                                                                                                                                                                           4254. .4995
Organism="Flaveria trinervia"
mol_type="other DNA"
/db_xref="taxon:4227"
                                                                                                                                                                                                           'organism="Escherichia coli
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/function="35S promoter"
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2865..4210
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/db_xref="taxon:10641"
                                                                                                                                                                                                                            /mol_type="other DNA"
/strain="K12"
   ., P.O. Box 1600, Ca
Location/Qualifiers
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/gene="pdk"
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775. .1635
/gene="amp"
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4254. .4995
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5049. .581
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Best Local Similarity
Matches 779; Conserva'
     C.S.I.R.O.
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PN JP 2002537790-A/156

PN JP 2002537790-A/156

CC CL2NAS, CONTALAY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC

CC ALPS

CC CL2NAS, CONTALAY, COL CL2NAL, L5, C12NAL, 21, C12NS/10, C12NIS/ PC

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Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning of
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RR 02-NAR-1999 US 60/12589,23-NAR-1999 US 60/126049 PR
RT 02-NAR-1999 US 60/136744
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Synthetic construct
Synthetic construct
artificial sequences.
I (bases 1 to 4208)
S Hartley, J.L., Brasch, M.A., Temple, G.F. and Chec, D.
Compositions and methods for use in recombinational cloning of nucleic acids
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PN JP 2002537790-A/157
PD 12-NOV-2002
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/organism="synthetic construct"
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PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC C12N15/09, CO7K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC 00, C12N5/00 CC pDONR204 CC n is any nucleotide CC n is any nucleotide FH Key his C-feature (1326)...(1326).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2424 AAATCCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTTGATCGG---ATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATC
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Key
Location/Qualifiers
misc_feature (1326). (1326).
Location/Qualifiers
1. .4165
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                               Score 989.6; DB 6;
Pred. No. 5e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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22.2%;
Best Local Similarity 98.8%;
Matches 1008; Conservative
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                                                                                                               1823 TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGG
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                   TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA
                                                5063 TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA
                                                                                                                                                                                     4943 AGGGAGCCTGACATTTATATTTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT
                                                                                                                                                                                                                                         TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGGATAACGGAGACCGGCACACTGGCCATA
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                                                                                          CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA
                                                                                                                                                               AGGCAGCCTGACATTTATATTCCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT
                                                                                                                                                                                                                                                                                                              TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGG
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I (bases I to 4165)

Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.

Compositions and methods for use in recombinational cloning
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JP 2002537790-A/158
12-NOV-2002
02-MAR-2000 JP 2000602252
02-MAR-1999 US 60/122389,23-MAR-1999 US
AY-1999 US 60/136744
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Patent: JP 2002537790-A 158 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/158
PD 12-NOV-2002
PF 02-MAR-2000 JP 2006602252
PR 02-MAR-1999 US 60/122389,23-MAR-19
28-MAY-1999 US 60/136744
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JP 2002537790-A/158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5303 IGITCITCGGGTGATGCTGCCAACTTAGTCGACGACAGCCTTCCAAATGTTCTTCTCAA 5244
                                                                                                                                                                                                                                                                                                                                                                                               OS ALIFECIAL Sequence
DN JP 2002537790-A/180
DN JP 2002537790-A/180
DD 12-WOV-2002
DP 12-WAR-2000
DP 02-MAR-1999 US 60/125389,23-MAR-1999 US 60/126049 PR
DS MAR-1999 US 60/136744
DI JAMES L HARTLEY MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA 325
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                                                                                                                                                                                                                                   synthetic construct
synthetic construct
artificial sequences.
1 (bases 1. Brasch, M. A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning of
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/organism='Artificial Sequence'.

Location/Qualifiers

1..5584

/organism="synthetic construct"

/mol type="genomic DNA"

/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                               nucleic acids
Patent: JP 2002537790-A 180 12-NOV-2002;
INVITROGEN CORP
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                                  4747
             4716 ATAGCACACCTCTTTTTGACATACTTCGGGTA
1106 ATAGCACACCTCTTTTGACATACTTCGGGTA
                                                                                                                                                                                                BD263402.1 GI:33073170 JP 2002537790-A/180.
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CC pDONR207
FH Key
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#1176 AGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 4235
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                                                                                                                                                                                                                                                                                                                                                                                                                                ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA
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                             3636 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATT
                                                                                                                     AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACAACATCCAGTC
                                                                                                                                                                   3696 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACAACATATCCAGTC
                                                                                                                                                                                                                                                                                                         TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTAA
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Pred. No. 3.4e-150;
0; Mismatches 2;
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/organism="synthetic cor
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 99.8%; Pred. No. 3.5e-150;
Matches 1110; Conservative 0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                          TATTATTACAAATCCAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTAAAAGACTGAT 18280
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Patent: JP 2002537790-A 155 12-NOV-2002;
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PF 02-MAR-2000 JP 200602252
PF 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR 28-MAY-1999 US 60/136744
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC
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JP 200253779.1 AI:33073145
JP 2002537790-A,155.
synthetic construct
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1 (bases 1 to 4470)
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning of
                                                                                 ATTIACTGATTGTACCCTACTACTTATATGTACAATATTAAAATGAAAACAATATATTGT
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	ADAICATTIAGGITICICATCAGGITICITGIACAAAGIGG	δy	
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Best Local Similarity 79.1%;
Matches 4406; Conservative
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Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
21461301
                                                                                                                                                                                                                                                                      note="pHELLSGATE is a derivative of cloning vector
                                                                                                                  Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Camberra, ACT 2601, AUSTRALIA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACACAATATCCAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATTT
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/gene="pdk"
/note="pyruvate orthophosphate dikinase (pdk)"
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/note="octopine esynthase (ocs) terminator"
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/function="35S promoter"
14660. .16258
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GenCore version 5.1.6
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OM nucleic - nu	nucleic search, using sw model
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Scoring table:	IDENTITY NUC Gapop 10.0, Gapext 1.0
Searched:	3470272 segs, 21671516995 residues
Total number of	f hits satisfying chosen parameters: 6940544
Minimum DB seq Maximum DB seq	length: 0 length: 200000000
Post-processing:	g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	9	47.	21.3	20	9	37	BD263379 Compositi
υ	7	82	18.5	20	φ	BD263378	BD263378 Compositi
υ	œ	•	18.5	15	9	8	BD263382 Compositi
	σ	7	17.5	82	12	CVE311872	AJ311872 Cloning v
	10		17.5	6063	12	187	AJ311873 Cloning v
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	13		16.8	7049	9	A23998	A23998 pTE4 expres
υ	14		16.5	10138	12	AF187951	AF187951 Activatio
	15		16.3	7566	9	~	A24783 plasmid pPS
	16		16.3	7566	ø	AR074388	AR074388 Sequence
	17		16.3	7639	Q	~	A24782 plasmid pJD
	18		16.3	7639	9	AR074387	AR074387 Sequence
	13		16.2	11405	12	AY310901	AY310901 Binary ve
	20		16.1	22574	12	CVE18556	Y18556 Cloning ve
	21		16.0	4947	9	Н	BD217610 Method an
υ	22		15.9	7599	9	AX063413	AX063413 Sequence
	23		15.9	5399	9		A18050 DNA for tra
	24		15.9	5399	9		AR095106 Sequence
	25		15.9	5399	φ	AR098312	AR098312 Sequence
	56		15.9	5399	φ	149885	149885 Sequence 1
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	32		15.9	14194	ø	AX052541	AX052541 Sequence
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ALIGNMENTS

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Pred. No. is the number of results predicted by chance to have a

1 Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q., Gooding,ps., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,

ORGANISM REFERENCE AUTHORS

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Length DB I I I I I I I I I I I I I I I I I I	Score Watch Length DB ID 3955.4 Match Length DB ID 1207.4 24.8 4470 6 BD263317 1207.4 24.8 4470 6 BD263317 1207.4 24.8 4470 6 BD263318 1207.4 24.8 4470 6 BD263318 1207.4 24.8 4470 6 BD263318 1207.4 24.8 4470 6 BD263318 1207.4 24.8 4470 6 BD263318 1207.4 24.8 4470 6 BD263318 1207.4 24.8 4470 6 BD263318 1207.4 24.8 4470 6 BD263318 1207.4 24.8 4593 6 BD263318 1207.4 24.8 5584 6 BD263318 1207.2 16.9 5126 6 BD263318 1207.3 16.9 16.9 5156 6 BD263318 1208.1 16.9 5156 6 BD263318 1209.6 15.0 7566 6 AR01438 1209.6 15.0 7566 6 AR01438 1209.7 14.6 1209 6 AR01631 1209.8 14.6 5399 6 AR01631 1200.8 14.6 5399 6 AR01631 1200.8 14.6 5399 6 AR01631 1200.8 14.6 5399 6 AR01631 1200.8 14.6 5	τ. 1			* 5			SUMMARIES		
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13360 AACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAA 13419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13240 CACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGGACAGCCTTCCAA 13299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13300 ATGITCTICGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCAA 13359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13000 TITCATITGGAGAGGACACGCTCGAGGCTAGCATGGATCTCGGGGCCCCCAAATAATGATTT 13059
                                                                                                                                                                                                                                                                                                                                                                                          AKRELQFGEWQRNDILAGIFEPATIDIDLAILLTKAREHSVALVGPAABELFDPVPEQ
DLFFALNETLTLMNSPPDWAGDERNVVLTLSRIWYSAVTGKTAPKDVAADWAVERLPA
YQQVILEARQAYLGQEDRLASRADQLEEFVHYVKGEITKVVGK"
10706. .11324
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GRLGVADRYQDIALATRDIABELGGEWADRFLVLXGIAAPDSQRIAFYRLLDEFF"
                                                                                                                                                                                                                                                                                                                                                        /trānslation="MREAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKP
HSDIDLLVTVTVRLDETTRRALINDLLETSASPGESEILRAVEVTIVVHDDIIPWRYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13120 TGCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATGATATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>TATTTTGACTGATAGTGACCTGTTGGTTGCAACAAATTGATGAGCAATGCTTTTTTATAA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TABATTTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACAAATATCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="pyruvate orthophosphate dikinase (pdk)"
                                                                                                                                                                                                                                      /codon_start=1
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/product="spectinomycin_resistance_protein"
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/db_xref="G1:15982220"
/db_xref="G1:15982220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="octopine esynthase (ocs) terminator"
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12 Score 3985.4;
13 Score 3985.4;
14 Pred. No. 0;
15 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="35S promoter"
14660. .16258
                                          1443. .2148
/note="NOS terminator"
2149. .2706
/note="left border"
7793. .9388
                                                                                                                                          'transposon="Tn7"
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gene="spec"
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gene="spec"
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/db_xref="REMTREMBL:CAC86252"
/db_xref="NAIL:LAGATSLEDISARIRAGSPAAWVERLFGYDWAQQTIGCSDAA/LTANS1ation="WAITTANDLSAFSLEJSARIRAGSPAAWVERLFGYDWAQQTIGCSDAAVREAGGREVLFWYFDLSGALNELQDEAARLSWLATTGVPCAAVLDVVTEAGRDWILL
LGEVPGQDLLSSHLABPAEKVSIMADAMRRLHTLDPATCPFDHQAKHRIERARTRMEAG
Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
                                                                                                                                                                                                                                                                                                                                       /note="pHELLSGATE is a derivative of cloning vector
pART27"
                                                                                                                                                            Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="neomycin phosphotransferase II (nptII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="kanomycin resistance protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Agrobacterium tumefaciens"
/mol_type="other DNA"
/mol_type="other DNA"
11674. .13019
                                                                                                                                                                                                                                                          /organism="Cloning vector pHELLSGATE"
|mol-type="other DRN"
|db xref="taxon:167049"
|lab_host="Escherichia coli"
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/organism="Flaveria trinervia"
/mol_type="other DNA"
/db_xref="taxon:4227"
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/mol_type="other DNA"
/db xref="taxon:562"
9389. 11673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 .448
/organism="Agrobacterium tu/mol_type="other DNA"
/db_xref="taxon:358"
449 .1442
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/function="NOS promoter"
448. .1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="other DNA"
/strain="K12"
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/db_xref="taxon:562"
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/db_xref="taxon:358"
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|gene="nptII"
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Waterhouse, P.M.
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                                                               JOURNAL
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14560 TTGCTTATCATTTGCTACGACGACCTATCAGTCAAAATAAAATATTTT 14619 1621 CCATCCAGCTGCAGCAATTCGGTACCCCAGCTTGGTAATAATTATTT 1680 14620 CCATCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCCAGCTTGGTAAGGAATAATTATT 1680 14620 CCATCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCCCA-ATTGGTAAGGAATAATTATT 14678 1681 TTCTTTTTCCTTTTAGTATAAAATAGTTAAGTGATTAATTA	1801 TAATGTAAAAAATATGACAAGTGATGTGTAAGACGAAGAAGAAGATGAAGATTGAGAGTAAG 1860 14799 TAATGTAAAAAAATATGACAAGTGATGTGTAAGAGGAAGAAGAAAGA	1915	1915 1914 15039 TATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCAGTCAG	1915 1914 15159 ACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAAT 15218 1915	1915 15279 1915 15339	1915 15399 ATTTCCCTAAAGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTT 15458 1915	1915
481 TATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAA 540 3480 IATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAA 13533 541 CTCTTATACATTTCTCTTACAAGTCGTCGGCTTCATCTGGATTTTCAGCCTCTATACTT 600 ACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGAATTTTCAGCCTCTATACTT 1359 601 ACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACTTGCAGCTGTGTAT 1359 660 ACTAAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACTTGCAGCTGTGTAT 1365 661 AAGGGAGCCTGACAATTTCTACTGTAATTTCTACTGTAATTGACCTGCAGACTGGCTGTTAT 1365 661 AAGGGAGCCTGACAATTTCTACTGTAATTTCTACTGTATTTTTATTGATGTTTTTTATTTCTACTGTATATTTTTATTTCCCCAGAACATCAGACTTGCTTTTTTATTTCTACTGTATATTTTTATTTCTACTGTATATTTTTATTTTATTTTATTTTATTTTTTTT		841 GGAGACTTTATCTGACAGCAGACGTGCCCCGGGAGGGATCACCACCGCGGGGGGGG	GGIGTARATARATATCACTATTCACCACTACTCTCGTCACACACACACACA	14020 TITCAATAAACCGGGCGACCTCCTCCTCCTGATTITCCGCTTTCCAGCGTTCGG 14079 1081 CACCCAGACGACGACGTTCATTCTGCATGGTTGTCCTTACCAGACATATTGACAT 1140 14080 CACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACAGA	14199 1260 14259 1320 14319	21 GTGATCTTCCGTCACAGGTATTTATTCGGCGCAAAGTGCGTCGGGTGATGCTGCCAACTT	TATCAGNACIONE DE LA CONTRACTION DEL CONTRACTION DEL CONTRACTION DE LA CONTRACTION DE

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CGTTGCAACAATTGATGAGCAATGCTTTTTATAATGCCAACTTTGTACAAAAAAGCTG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGCTAGCATGGATCTCGGGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u> ACGCTAGCATGGATCTCGGGGCCCCAAATAATGATTTTTATTTTTGACTGATAGTGACCTGTT</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4470;
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Pred. No. 9e-167;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                         1. .4470
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

24.8%;

Best Local Similarity 99.9%;

Matches 1208; Conservative 0
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S Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
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L Patent: JP 2002537790-A 159 12-NOV-2002;
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PP 12-NOV-2002
PP 2002537790-A/159
PP 02-MAR-1999 US 60/12389, 23-MAR-1999 US 60/126049 PR 28-MAY-1999 US 60/136744
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                           CGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTA
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DN JP 2002537790-A/180
PD 12-NOV-2002
PP 02-NAR-1999 US 60/126049 PR 28-MAY-1999 US 60/126049 PR 28-MAY-1999 US 60/126344
PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/00 CC DDONR207
FM Key L. :5584
FT source /organism='Artificial Sequence'.
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             4379 IGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTAC
                                                          ATCCACAAACAGACGATAACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTC
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In that the sequences.
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning
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/ organism="synthetic construct" | mol type="genomic DNA" | db_xref="taxon:32630"
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Patent: JP 2002537790-A 180 12-NOV-2002;
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JP 2002537790-A/157.
Synthetic construct
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I (bases 1 to 4208)
Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning of
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                                                                                                            TTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTT
                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGACGTGCACTGGCCAGGGGATCACCATCGGTCGCCCGGGCGTGTCAATAATATCAC
                                          2468 TTTGGCGAAAATGAGACGTTGTGGCA----CATTTCACAACTCTTATACTTTTCTCT
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            TITIGGCGAAAATGAGACGITGATCGGCACTACCCATITCACAACTCTTATACTITITCTCT
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Patent: JP 2002537790-A 157 12-NOV-2002;
INVITROGEN CORP
OS Arnificial Sequence
NP JP 2002537790-A/157
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PN JP 2002537790-A/158
PD 12-NOV-2002;
PP 02-MAR-2000
PF 02-MAR-1999 US 60/126049 PR 28-MAR-1999 US 60/126049 PR 28-MAR-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC C12N15/09, COTK14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/00
CC pDONR204
CC n is any nucleotide
FH Key FT misc f-
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Compositions and methods for use in recombinational cloning of nucleic acids.
                                4440 GCTGTCGCTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA 4381
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                                                                                                                                                                                                                                                                                       synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 4165)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning of
GCTGTCGCTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="synthetic construct"
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JP 2002537790-A/158.
                                                                     CTTCGGGTA 1233
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Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, ps., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene silencing in plants
Plant J. 27 (6), 581-590 (2001)
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                                  3870 AGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATC 3929
                                                                                                                                                                                                                                                                                                                         3990 GACAGCAGCACTGCTACTGGCCAGGGGATCACCATCCGTCGCCGGGGGGTGTCAATAATA 4049
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                                                                                                                                                                                                                                                                                         GACAGCAGACGTGCACTGGCCAGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                  974 AACTIGCATTITCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCG
         AAGTITICIGIAATITICIACIGIATICGACCIGCAGACTGGCTGTGTATAAGGGAGCCTGAC
                                                                                                                                                                                                                     794 ATGCGCCAGCTTTCATCCCCCGATATGCACCGCGGTAAAGTTCACGGGAGACTTTATCT
                                                                                                                                                   734 AGATCAGCCACTICTICCCCGATAACGGAGACCGGCACACTGGCCATAICGGTGGTCAIC
                                                                             ATTTATATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTTTCGCGGTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ311874.1 GI:15982218 kanomycin phosphotransferase II; kanomycin resistance protein; gene; promoter; speC gene; spectinomycin resistance protein; transposon Tn7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 18691)
Waterhouse, P.M.
Direct Submissor 100 Waterhouse P.M., Plant Industry,
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers

    .18691
    /organism="Cloning vector pHELLSGATE" /mol_type="other DNA"
    db xref="taxon:167049"
    /lab_host="Escherichia coli"

    .264
    /organism="Escherichia coli K12"
/mol type="cuher DNA"
/strain="K12"

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PD 12-NOV-2002
PP 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/126049 PR 28-MAY-1999 US 60/126049 PR 28-MAY-1999 US 60/136744
28-MAY-1999 US 60/136744
C121NIS/09,C07K14/00,C12NIJ/15,C12NIJ/19,C12NIJ/21,C12NS/10,C12NIS/PC 00.C12NIS/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 TATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAAAGAAATAAAAA 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
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                                                                                                                                                                                                                                                               location/Qualifiers
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te (251). (131)
te (1158). (2082)
te (1509). (2082)
te (2251). (3130)
te (3174). (3464)
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                                                                                                           orthophosphate dikinase (pdk)"
                                                                                                                                                                                                            Length 18691;
                                                                                                                                                              terminator"
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                                                                                                                                                                                                            Score 842; DB 12;
Pred. No. 1.5e-113;
0; Mismatches 765;
                                                                                                                                                                /note="octopine esynthase (ocs)
              11674. 13019
/function="35S promoter"
14660. 16258
note="right border"
                                                                                                                  note="pyruvate
                                                                                 16258
                                                                                                                                  /number=2
17922. .18687
                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.7%;
Matches 1406; Conservative
                                                           /gene="pdk"
14660. .1625
                                                                                                 gene="pdk"
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HSDIDLLYTVTVRLDETTRRALINDLLETSASPGESEILRAVEVTIVVHDDIIPWRYP
ARRELOPGEWGRNDILAGIFEPATIDIDLAILLTRAREHSVALVGPAREELFDPVPBQ
DLFEALNETTIAWSPPDWAGDERNVVITLSRIWYSAVTGKTAPKDVAADWAMERLPA
QYOPVILEARQAYLGGEDRLASRADQLEEFVHYVKGEITKVVGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="WAITLSAYSLPISARIRAGSPAAWVERLFGYDWAQOTIGCSDAA
VFRLSAQGREVLFVKTDLSCALNBELODBAARLSWLATTGVFCAVLDVVTRAGRDWLL
LGSTGEODLDELSSHLAPAEKVSIMADAWRRLHTLDPATCPFDHQAKHRIERAATRWEAG
LVDQDDLDERHQGLAPAELFARLKARNPDGEDLVVTRGDACLENIWGRGREGGFIDG
GRLGVADRYQDIALATRDIABELGGEWADRFLVLYGTAAPDSQRIAFYRLLDEFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nptII"
/note="neomycin phosphotransferase II (nptII)"
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product="spectinomycin resistance protein"
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product="kanomycin resistance protein"
protein id="CAC86252.1"
| Dx.ref="G1:15982219"
| db_xref="REMTREMBL:CAC86252"
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/mol_type="other DNA"
/db_xref="taxon:358"
264. .447
                                                                                                                                                                                                                                                                                                        organism="Agrobacterium tumefaciens"
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/mol_type="other DNA"
/db_xref="taxon:358"
                          265. .448
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                                                                                                                                                                                                                                                                                                                                                                           'organism="Cauliflower mosaic virus"
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Flaveria trinervia"
/mol_type="cther DNA"
| Lib xref="taxon:4227"
| 179<u>7</u>2. .18691
                                                                                                                                                                                                   7793. 9388
/organism="Escherichia coli"
/mol_type="other DNA"
/db_xref="taxon:562"
9389. 11672
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db xref="GI:15982220"
db_xref="REMTREMBL:CAC86253"
                                                                                                        'organism="Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'function="NOS promoter"
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/note="NOS terminator"
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/note="left border"
/ros-.9388
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/db_xref="taxon:562"
                                                          /mol_type="curc."
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/transposon="Tn7"
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transl_table=
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/gene="nptII"
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/transl_table=
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/gene="spec"
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15824 TICTIAITTITACTAIAGIAITTIATCAITGAIAITTIAATTCAICAACCAGCIAGAAIT 15765
BD263378 4204 bp DNA linear PAT 17-JUL-2003 Compositions and methods for use in recombinational cloning of nucleic acids.
                                                                                                                                                                                                           artificial sequences.
1 (bases 1 to 4204)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning of
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                                                          AATTAAATATCTATACCATTACTAAATATTTTAGTTTAAAAGTTAATAAATTTTTGTTA
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Location/Qualifiers
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TITLE
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KEYWORDS
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                                                  17084 Acacecceesesacssarssarscanterice de la Acacecerca de la 17025
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                                                                                       CCACAAACAGACGATAACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCAC 986
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                   CACTGGCCAGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACAT
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LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKKPSRIVVIYTTGSQATMDERNRQIA
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                                                                                                                                                                                                                                                                                              /note="pHANNIBAL is a derivative of cloning vector pART7 which was a derivative of pGEM-92f(-)"
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                                                                                                 Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
1. .5824
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96.7%; Pred. No. 7e-111;
Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumefaciens"
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                                                                                                                                                                                                 PHANNIBAL"
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/note="octopine esynthase (ocs)
                                                                                                                                                                                                                                                                                                                                                                /organism="Escherichia coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4254. .4995
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                                                                                                                                                                                                 /organism="Cloning vector pH.
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/mol_type="other DNA"
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2865. .4210
(6), 581-590 (2001)
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/function="35S
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/gene="amp"
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/gene="amp"
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2 (bases 1 to 5824)
Waterhouse, P.M.
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Construct design for efficient, effective and high-throughput gene silencing in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3544 TITCCAGCGITCGGCACGCACGACGACGGCTTCAITCTGCATGGTGGTGCTTACCAGACC 3485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITCCAGCGTTCGGCACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACC 1126
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                                                                                                                                                                                            GAACAATITCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCACTGGATTTT
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                                                1204 TATTAAATCATAAAAAAAATAAGAAAAAAAGAGGTGCGAGGCCTCTTTTTTGTGTGACAAAA
                                                                                       TAAAAACATCTACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAA
                                                                                                                             raaaaacarcraccrarrcararacecragrercaragrercreaaaarcarcrecarcaa
                                                                                                                                                                     GAACAATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTT
                                                                                                                                                                                                                                                    CAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCA
          TATTAAATCATAAAAAAAATAAGAAAAAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAAA
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/product="kananycin resistance protein"
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EDTPFKDPREINTDFKTEKTERPEELVFSHGDLGDSNIFVKDGKVSGFIDLGRSGRADKW
YDIAFCVRSTREDIGEEQYVELFFDLLGIKFDWEKIKYYILLDDELF"
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              Watchbuse_P.M.
Direct Submission
Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.1.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
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/organisma-Agrobacterium tumefaciens"
/mol_type="cther DNA"
/db_xref="taxon:358"
/075. .1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mosaic virus"
                                                                                                                                                      /organism="Cloning vector pKaNNIBAL"
/mol type="tother DNA"
/db xref="taxon:167048"
/lab_nost="Bscherichia coli"
                                                                                                                                                                                                                                                                                                                         l. .3103
/organism="Escherichia coli K12"
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/mol_type="other DNA"
/db_xref="taxon:4227"
528B. .6053
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/function="358 promoter"
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/organism="Cauliflower mc
/mol type="other DNA"
/db_xref="taxon:10641"
4493. .5234
                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:83333"
3104. .4449
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/strain="K12"
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/note="octopine
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/gene="pdk"
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/gene="pdk"
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Construct design for efficient, effective and high-throughput gene silencing in plants
Plant G. 27 (6), 581-590 (2001)

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Cloning vector pKANNIBAL
Cloning vector pKANNIBAL
artificial sequences; vectors.
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PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC 00, C12NS/00

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CC May be any nucleotide

CC May be any nucleotide

FF Key

Location/Qualifiers

FT misc_feature (102) . (102)

FT misc_feature (102) . (3080).
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llarity 99.8%; Pred. No. 8.2e-111;
Conservative 0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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synthetic construct
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artificial sequences.
1 (bases 1 to 5156)
Hartley, J., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning
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Patent: JP 2002537790-A 160 12-NOV-2002;
INVITROGEN CORP
OS Artificial Sequence
PN JP 2002537790-A/160
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US
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Rosche, E., Streubel, M. and Westhoff, P.
Primary structure of the photosynthetic pyruvate orthophosphate
primary structure of the photosynthetic pyruvate orthophosphate
dikinase of the C3 plant Flaveria pringlei and expression analysis
of pyruvate orthophosphate dikinase sequences in C3, C3-C4 and C4
Flaveria species
Plant Mol. Biol. 26 (2), 763-769 (1994)
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Flaveria trinervia
Flaveria trinervia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bopernatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Tageteae; Flaveria.
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9324. 10401. 10580,
10735. 10872. 10947. 111111221. 11382,1480. 11569,
11673. 11811,11897. 12074,12295. 12424,12514. 12642,
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Molekular-, biologie der Pflanzen, Heinrich-Heine-Universitaet,
Universitaetsetr. 1, 40225 Duesseldorf, FRG
Location/Qualifiers
  422 ITTAAAAGTTAATAATATTTTGTTAGAAATTCCAATCTGCTTGTAATTTATCAATAAAC
                                                                                                                        2198 AATGTAACAAAACATAATCTAATGCTAATATAACAAAGCGCAAGATCTATCATTTTATAT
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F.trinervia pdk gene for pyruvate,orthophosphate dikinase.
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/organism="Flaveria trinervia"
/nol_type="genomic DNA"
/db xref="texon:4227"
/clone="inFtrpdk, inFtrpdkA-F"
/fissue type="full expanded leaves"
/clone_lib="lambda Dash, lambda ZAPII"
1212. .14264
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/gene="pdk"
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                                                                                                                          17-JUL-2003
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                                                                                                                                                                                                                         synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 786)
Waterhouse, P.M., Wang, M.B. and Graham, M.W.
Method and means of obtaining improved phenotype
Patent: JP 2002511258-A 7 16-APR-2002;
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
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4376 GTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTA 4330
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g improved phenotype
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Similarity 100.0%; Pred. No. 2.7e-104;
00; Conservative 0; Mismatches 0;
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                                                                                                                      Method and means of obtaining BD194641
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JP 2002511258-A/7.
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VPLVGTPQELRHQI SVIRGVAANVFAEMGVTLEYKVGTMI EI PRAALI AEEI GKEADF
FSFGTNDLTQMT FGYSRDDVGKFLQI YLAQGILQHDPFEVI DQKGVGQLI KMATEKGR
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NAQGEDVVAGIRTPEDLGTMETCMPEAYKELVENCEILERHYKDMMDIEFTVQENRLW
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VRGMNGNISGTGVLFTRNPSTGEKKLYGEFLINAQGEDVVAGTRIPBDLGTMETOMPE
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                                                                                 Gaps
                                                                                0;
                                                                Length 14645;
                                                                                 Indels
                                                              Score 778.6; DB B;
Pred. No. 2.7e-104;
0; Mismatches 9;
/gene="pdk"
/number=13
11673. .11811
/gene="pdk"
/number=13
                                              11812. .11896
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98.9%;
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18-JAN-1995

PAT

linear

DNA

7049 bp

A23998 pTE4 expression vector A23998

RESULT 14
A23998
LOCUS
DEFINITION
ACCESSION

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                                                                                              Sevcik, J.
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synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 7049)
Nazarov,V., Botterman,J., Stanssens,P. an
A novel ribonuclease and its inhibitor
Patent: EP 0537399-A 3 21.APR-1993;
PLANT GENETIC SYSTEMS, N.V
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                                                                                                                                                                                                                                                      DNA"
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/organism="synthetic c
/mol_type="unassigned
/db_xref="taxon:32630"
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BWTDDLVRLRERYPWLVAEVDGEVAGIAYAGPWKARNAYDWTAESTVYVSPRHQRTGL
GSTLYTHLLKSLEAQGFKSVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene promoter enhancer
                              SYN 11-MAY-2000
                                                                                                                                                                                                                                                                                                     Z (bases 1 to 10138)

Kardailsky, I. and Weigel, D.

Direct Submission

Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA
                                                                                                   Activation-tagging vector pSK1015
Activation-tagging vector pSK1015
artificial sequences; vectors.

1 (bases 1 to 1013)
Weigel, D., Ahn, J.H., Blazquez, M.A., Borevitz, J.O.,
Christensen, S.K., Fankhauser, C., Ferrandiz, C., Kardailsky, I.,
Malancharuvil, E.J., Neff, M.M., Nguyen, J.T., Sato, S., Wang, Z.,
Xia, Y., Dixon, R.A., Harrison, M.J., Lamb, C.J., Yanofsky, M.F. and
Chozy, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to glutamine synthetase
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                              DNA linear complete sequence.
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/mol_type="genomic DNA"
/mol_type="taxon:109189"
2.xref="taxon:109189"
12...31
/note="T7 RNA polymerase promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830. .2849
note≂"T7 RNA polymerase promoter"
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Plant Physiol. 122 (4), 1003-1013 (2000)
20223715
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/note="5' end and promoter"
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/note="derived from phage f1"
2663. .2829
/note="derived from pUC19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7690. .7713
/mote="T-DNA left border"
complement (8054. .8784)
/product="octopine synthase"
/note="a" end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (<8785. .>9420)
complement (8791. .9342)
/note="promotes resistance
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4270. 4294
/note="T-DNA right border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="dervied from pUC19"
                               AF187951
Activation-tagging vector pSKI015,
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db_xref="GI:6537290"
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transl table=
                                                                         AF187951.1 GI:6537289
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RESULT 15
AF187951/c
LOCUS
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ACCESSION
VERSION
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CDS
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JOURNAL
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PUBMED
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15.1%; Score 735; DB 12; 100.0%; Pred. No. 6.7e-98; tive 0; Mismatches 0;

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fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be ded to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of mucleic acids. The present sequence represents an acceptor vector nucleotide
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria auch as Bacherichia coll; (b) selectable marker region capable of being expressed in the recipient cell c selectable marker region capable of being expressed in the recipient cell c region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerases (iii) first, second, third and courth recombination sites, (iii) first, second, third and courth recombination sites, or the second and third recombination sites, or the second and third recombination sites, or the first and second recombination sites, or the third and fourth recombination sites, do not recombination site, or the third and courth recombination site. The vector is used for silencing target nucleic cald sequences. The vectors an also be used to convert a DNA fragment tite on inverted repeat structure. Plants transformed with a vector from the present invention of the phenotypic expression of mucleic chimeric gene for reduction of the phenotypic expression of mucleic acids. The present invention
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                                                                                                           New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u> AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACACATATCCAGTC</u>
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92.2%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                            Claim 17; Page 93-102; 104pp; English.
                                    Helliwell
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                                  Waterhouse P,
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                            CGGTTTCGGTTCATTCTAATGAATATATCACCCGTTACTATCGTATTTTTATGAATAATA 16874
                                                                                                                                                                              CAATATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGAGGCGCACAATAAAA 16994
                                                                                                                                                                                                                                                                                                                                            17055 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTAC 17114
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                                                                                                                                                   CAATATATTGTGCTGAATAGGTTTTATAGCGACATCTATGATAGAGCGCCACAATAACAAA
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                                                                                                                                                                                                                                                               16995 CAATTGCGTTTTATTATTACAAATCCAATTTTAAAAAAGCGGCAGAACCGGTCAAACCT
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CTRAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 1 GGGGAGCCTGATTAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGCTGCTGTATA 1 AGGGAGCCTGATTAAATTCTGCCAAACATCAGGTTAATGGCGTTTTTGATGTCATTT 7 AGGGAGCCTGACATTTATAATTCCCCCAAACATCAGGTTAATGGCGTTTTTTGATGTCATTT 1 AGGGAGCCTGACATTTATAATTCCCCCAAACATCAGGTTAATGGCGTTTTTTGATGTCATTT 1 TCGGCGGTGGCTGACATTATATTCCCCCCAAACATCAGGTAAATGGCGTTTTTTTAATGTCATTT 1 TCGGCGGTGGCTGACATCATCACCCCCCAAACATCACCGACGCGCAACTGGCCATA 1 TCGGCGGTGGCTGACATCACCCCCCAAACATCACCCACCGGGCAACTGGCCATA 1 TCGGTGGTCAATAATTATCACTGCCCCCTTTCATCCCCCGAATAACGGACCACTGGCCATA 1 TCGGTGGTCAATAATATCACTGTACACTCCACAAACAGACGAACACTGCCCATCATTAATAACTGGTCATTAATAACTGCACTAGCCACTCACT	1382 GTGACTACGGTCACTAATACCATCTAAGTGATGATGATGATGTGATGTTGTT 14186 GTGGACTACGGATATCTCATACTAGTGATGTTGT 14186 GTGGACTACAGGTCACTAATACCATCTAAGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT

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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia col; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter cell or by prokaryotic RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerases; (ii) first, second, third and fourth recombination sites; or the second and third recombination sites; or the second and third recombination sites; are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination site, or the third and court recombination sites, do not recombination site, or the third and same recombination site, The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to the present invention and the same characteristics or to introduce and the converted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to the present invention and the same characteristics or to introduce and the present invention and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same characteristics or to introduce and the same chara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-
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                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.
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                                                                                                                                                                                                                                                                                                                                    sequence SEQ ID NO:25
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                                                                                                                                                                                                                                                                                                                                    Acceptor vector PHELLSGATE 11 nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; Page 83-93; 104pp; English.
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                                                                                       ABQ82142 standard; DNA; 17458 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.
                                                                                     GCAGCATITITITIGGGGTGTATGGGGGCCCCAAATGAAGTGCAGGTCAAAACCTTGACAGTGA
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                                                                                 TACGCTGCTTCATAGCACCACCTCTTTTTGACATACTTCTGTTCTTTGATGCAGATGATTTTT
                                                                                                         GAGGCTCGCACCTCTTTTTTTTTTTTTTTTATATACGGCATTGAGACAATA
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fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target mucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimetic gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide
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                                                                                                                                                                                                                                                                                                                                                           1 TITCAILITGGAGAGAGACACGCTCGAGGCIAGCAIGGAICTCGGGCCCCCAAAIAAIGAITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TABATTAGATTTTGCATABABACAGACTACATAATACTGTABAACACAACATATCCAGT
                                                                                                                                                                                                                                                                                                                  831; Gaps
                                                                                                                                                                                                                                    Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                         Score 3985.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                               sequence from the present invention
                                                                                                                                                                                                                                                                         similarity 85.1%;
5: Conservative C
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	ठे र्	961 (GGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCA 1020
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<u>-</u>	<i>₹</i> 5	1201	CATAGCACACTCTTTTTGACATACTTCGGGTAGTGCCGATCAACGTCTCATTTTCGCCA 1260
_	δ	1261	AAAGTIGGCCCAGGGCTICCCGGTATCAACAGGGCACACCAGGATTTATTTATTTATGGCGAA 1320
	qq	09	GCCCCAGGGCTTCCCCGGTATCAACAGGGACACCAGGATTATTTAT
	OY DP	1321	GIGATCTICCGICACAGGIATITAITCGGCGCAAAGIGCGTCGGGGGAIGCIGCCAACTI 1380
	ò 1	381	AGTICAACTACAGGICACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGATATGTTG 1440
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	% d	1501	TATATCATTITACGITTCTCGTTCAGCTTTCTTGTACAAGTTGCCATTATAAGAAAGCA 1560
	8 8	561	TIGGTTATCAATTIGTIGCAAGGAAGGGTCACTATCAGTCAAAATAAAAT
	ò	621	TCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCCAGCTTGGTAAGGAAATAATTATT 1680
<u></u>	අ <u>ද</u> ි	14620	CCATCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCCA-ATTGGTAAGGAAATAATTATT 14678 TTCTTTTTCCTTTTAGTATAAATAGTTAAGTGATGTTAATTAGTATGATTATAATA
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ATCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACG

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13660 AAGGGAGCCTGACATTTATATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATT 13719

AAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTGATGTCATT

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13600 ACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTAT

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CTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTT

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CTCTTATACTTTTCTCTTTACAAGTCGTTCGGCTTCATCTGGATTTTTCAGCCTCTATACTT <u> ACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTAT</u>

15999 ATATCAAACTAATAGAAACAGTAATCTAATGTAACAAAACATAATCTAATGCTAATAA 16058 2231 CAAAGCGCAAGATCTATCATTTATATAGTATTATTTTCAATCAA	2291 CTABATAGTIGTAGTITTATTAACTICTAAATGGATTGACTATTAATTAAATGAATT 2350	2351	16179	2411 TACATTTGGATTGATTACAGTTGGGAAGCTGGGTTCGAAATCGATAAGCTTGGATCCTCT 2	18239 TACATTIGGATIGATIAATTACAGTIGGGAAATTGGGTTCGAAATCGATAAGCTTGGATCCTCT 2471 BGAGBGCTGCBGCTGGBARAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	16299 AGAGAGCTGCAGCTGGCAAATAATGATTTTATTTTGACTGATAGTCGTTCGT	y 2531 TGCAACAAATTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGGTGAAC 2590	2591 GAGAAACGTAAAATGATAAATATCAATATTAAATTAGATTTGATTTGATTTGATAAAAAAAA	16419	2651 CTACATAATACTGTAAAACACAATATCCAGTCACTGATGAATCAACTACTTAGATGGTA 2710	164/9 CIACAIACIGIAAAACACAACAIAICCAGICACIAIGAAICACTAGAIGGIA 165	Y 2711 TTAGTGACCTGACTAAGTTGACACCACCGACGCTTTGCGCGCGAATAAA 2770 16539 TTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCCGACGCACTTTGCGCCGAATAAA 16598	2771	b 16599 TACCTGTGACGGAAGATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACCG 16658	2831 GGAAGCCTGGGCCAACTTTGGCGAAAATGAGACGTTGATCGGCACTACCCATTTCACA 2890	16659 GGAAGCCCIGGGCCAACTTTGGCGAAAATGAGACGTTGATCGGCACTATTCACA	y 2891 ACICITALACHILCICITACAAGICGTICGGGTICATCIGGGTITICAGCCICITALACT 2950 16719 ACICITATACITITICICITACAAGICGTICGGCTICATCIGGATITICAGCCTCTATACT 16778	2951 TACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTA 3	16779 TACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTA	3011	y 3071 TTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCA 3130	Y 3131 TATCGGTGGTCATCAGCGCCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCAC 3190	3191 GGGAGACTTTATCTGACGAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGG 3250	17019 GGGAGACTTTATCTGACAGCAGACGTGCACGTGGCCAGGGGGATCACCATCCGTCGCCCGG 17	y 3251 GCGFGTCAATAATATCACTCTGTACATCCACAAACAGCGATAACGGCTCTCTTTTAT 3310
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14919 CCAACTTTCACCATAATGAAATAAGATCACTACCGGGCGTATTTTTGAGTTATCGAGAT 14978 1915 1914 14979 TTTCAGGAGCTAAGGAAGCTAAAAATGGAGAAAAAATCACTGGATATACCACGFTGATA 15038	191	15039 TATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCAGTCGGTTGCTCAATGTACCT 15098	ATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAAAAA	1915 1915	15159 ACAAGITTIAICCGGCCTITAITCACATTCTTGCCCGCCTGAIGAAIGCTCAICCGGAAI 15218	1915 1914 15219 TCCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGGATAGTGTTCACCCTTGTTACA 15278	1	15279 CCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATT 15338	1914 15339 TCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCT 15398	191	15399 ATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTT 15458	6	LACCAGITITAAACGIGGCCAATAIGGACAACTICITCGCCCCCGTTTTCACCA	15519 TGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATC 15578		15579 ATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCG 15638	н .			1931 AATAGTAATTCTAGCTGGTTTGATGAATTAAATATCAATGATAAAATACTATAGTAAAAA 1990 	1991 TAAGAATAAATAAAATAAAATAATATTTTTTATGATTAATAGTTTATTA	TATCTATACCATTACTAAATATTTTAGTTTAAAAGTTAATAAATA	TATCTATACCATTACTAAATATTTTAGTTTTAAAAGTTAATAAATA	2111 CARTICULGURATITATOARIAACAAAATATTAARIAACAAGGTAAAGTAACAAATA 2170 	2171 ATATCAAACTAATAGAAACAGTAATCTAATGTAAACATAATGTAATGCTAATATAA 2230
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nucleotide sequence. Also described are: (1) an isolated nucleic acid
nucleotide sequence. Also described are: (1) an isolated nucleic acid
an least one mutation in its core region that increases the specificity
of interaction between the recombination sites and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (1), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, oleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing (I), (II), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is used
in the exemplification of the present invention
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Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

144 264 244 324 364 444 504 564 544 624 604 684 664 CCAGAACAICAGGITAAIGGCGITITITGAIGTCAITITCGCGGIGGCIGAGAICAGCCAC 744 124 204 184 304 384 424 484 64 GCCTCTTTTTTGTGTGACAAATAAAAACATCTACCTATTCATATACGCTAGTGTCATAG CGTTGCAACAAATTGATGAGCAATGCTTTTTTATAATGCCAACTTTGTACAAAAAGCTG AACGAGAAACGTAAAATGATATAAATATCAATATATTAAAATTAGATTTTGCATAAAAAC crinaticaccacacaccriccaargircricricaaacagaarcarcaaccaa CTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAAGAAATAAGAAAAAAGGGTGCGA GCCTCTTTTTTGTGTGACAAAAAAAAAACATCTACCTATTCATATACGCTAGTGTCATAG TCCTGAAAATCATCTGCATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGT TCCTGAAAATCATCTGCATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGT cerrosectricarcrosaritricascercraracritacianaacertaaaserricrora ATTICIACIGIATCGACCIGCAGACIGGCIGIGIAIAAGGGAGCCIGACATTIAIATICC ATTICTACTGTATCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCC Acectaecarecarcececcoaaaraarearrirarriraacearaarearerer CGTTGCAACAATTGATGAGCAATGCTTTTTTTATAATGCCAACTTTGTACAAAAAAGCTG AACGAGAAACGTAAAATATAAATATCAATATTAAATTAGATTTTGCATAAAAAAC AGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATG 185 AGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATG GTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAA GTATTAGTGACCTGTAGTCGACCGACACCCTTCCAAATGTTCTTCGGGTGATGCTGCCAA CITAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTA CGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTAAACGTGATAAAGTTTCTGTA 25 AGGCTAGCATGGATCTCGGGCCCCCAAATAATGATTTTAATTTTGACTGATAGTGACCTGTT Gaps Score 1207.4; DB 3; Length 4470; Pred. No. 1.6e-164;); Mismatches 1; Indels 0; 0; 24.8%; Matches 1208; Conservative Local Similarity 545 145 125 365 485 265 605 Ŋ 85 65 205 245 325 385 445 425 505 265 305 Dp. ð Op à g ð 셤 à g ag ò Db g $\frac{7}{2}$ d à à g g δ à à

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985 ACCAGICCCIGIICICGICAGCAAAAGAGCCGIICAIIITCAAIAAACCGGGGGACCICAG 1044
                                                                                                                                                                                                                                                                                                                    CCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGACGACGGCGTTCATTCT 1104
                                                                                                                                                                                                                                                                                                                                                                         GCATGGTTGTGCTTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATA 1164
                                                                                                                                                                                                                                                                                                                                                                                                   GCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATA 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                1145 GCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATA 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
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                                                                                              TTCATCCCCGATATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moving an insert nucleic acid between vectors using site-specific recombination in vivo, useful for studying the biology of the organism, including array construction, reporter gene fusions, mutagenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises a method for moving an insert nucleic acid molecule between vectors, the method involves moving an insert nucleic acid from one vector to another using site-specific recombination. The
  TTCATCCCCGATATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACG
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                            The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid comprising one or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid will a second population; (b) mixing the second population of nucleic acid will a second population of the second population to or all of the nucleic acid molecules of the second population to or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence
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26B-C; 273pp; English.
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Best Local Similarity 99.9%;
Matches 1208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least come mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
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                                                                   965 ACCAGTOCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGGGGACCTCAG
                                                                                                                CCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGGCGACGACGGCCTTCATTCT
                                                                                                                                                                                       GCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATA
                                                                                                                                                                                                                         1085 GCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATA
                                           ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAG
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useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding an attBl, attLl, attL2, attRl, and attR2 nucleotide sequence recombinational cloning of polypeptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC55525 standard; DNA; 4939 BP.
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comprising a second recombination site that interacts with the mutated at recombination site. (1), (11), primers, vectors and methods from the present invention are used for the recombinational clouds from the present invention are used for the recombinational clouding of nucleic acid molecules. They can be used for changing vectors, targeting desired proteins, or intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to changing copy number, changing replicons, clouding into phages and clouding. (1), (11), (111), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used
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Best Local Similarity 99.9%;
Matches 1208; Conservative
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                                                                                                                                                                                                                                                                                            4679 GCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATA
                                                                                                                                                                                                                    GCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATA
TECACTGGCCAGGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTAC
                     1379 IGCACTIGGCCAGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTAC
                                                    ATCCACAAACAGACATAACGGCTCTCTTTTATAGGTGTAAACCTTAAAACTGCATTTC
                                                                              4439 ATCCACAAACAGACGATAACGGCTCTCTTTTTATAGGTGTAAAACCTTAAAGCTGCATTTC
                                                                                                          ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAG
                                                                                                                                    ACCAGTCCCTGTTCTCGTCAGCAAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAG
                                                                                                                                                               CCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGGACGACGACGTTCATTCT
                                                                                                                                                                                 CATCCTTCCTGATTTTCCGCTTTTCCAGCGTTCGCCAGACGACGACGGCTTCATTCT
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at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att combination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising to mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (III), withers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting generated proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cleaving into phages and cloning. (I), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention
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4741 1044 1164 4441 1224 4801 4681 4621 4561 1104 4501 4440 GCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATA 4381 864 924 984 Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid. The invention relates to inserting a population of nucleic acids into a TTCTTCCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCT GCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATA GCTGTCGCTGTCAACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATA TICAICCCCGAIAIGCACCACCGGGIAAAGIICACGGGAGACITIAICIGACAGCAGACG Trcarcccccararccaccaccccccaraacricacccccacrirarcrcacacaccc TGCACTGGCCAGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTGTAC 4740 recacredecadedegarcaccarcedececedegedrereararareacererae ATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTC ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACGGGGGGACCTCAG ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAG CCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGACGGGCTTCATTCT 4560 CCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCCAGACGACGGCTTCATTCT recombination, nucleic acid selection; ds. DRN; Byrd Donor plasmid pDONR207 nucleotide sequence.

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second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population, (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the donor plasmid pDONR207 nucleotide sequence
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Pred. No. 1.6e-164;
0; Mismatches 1;
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Best Local Similarity 99.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population, (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
                                    984
                                                                                                                                                                                      CCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGACGACGACGGCTTCATTCT
                                                                                                                                                                                                                                   GCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGTGTT
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                                                                                                  <u>ACCAGTCCCTGTTCTCGTCAGCAAAAGGCGGTTCATTTCAATAAACCGGGCGACCTCAG</u>
                                                                                                                                  Accadrocordirorocadadadadocorrocarradadocogocodocoros
                                                                                                                                                                   Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; ds.
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population for nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence
   1742 ATCCACAAACAGACGATAAGGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTC 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.
                                                                                                                                                                                                    GCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATA
                                     ACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAG
                                                                  1802 ACCAGICCCIGIICICGICAGCAAAAGAGCCGIICAIITICAAIAAACCGGGCGACCICAG
                                                                                                       CCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGGACGACGACGGCTTCATTCT
                                                                                                                             GCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATA
                                                                                                                                                                                                                                            GCTGTCGCTGTCACTGTCACTGTAATACGCTTCATAGCACCCTCTTTTTGACATA
                                                                                                                                                                                                                                                                              GCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents the destination plasmid pDONR212(F) nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombination; nucleic acid selection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTAC 1741
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recombine with some or all of the second target nucleic acid molecules form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR212 nucleotide sequence
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                                                                                                                                                                                          25 AGGCTAGCATGGATCTCGGGCCCCCAAATAATGATTTTTATTTTTGACTGATAGTGACCTGTT
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                                                                                                                                                        0;
                                                                                     Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 U; 0 Other;
                                                                                                                       Length 4428;
                                                                                                                                                      Indels
                                                                                                                                                        S.
                                                                                                                      Score 1201; DB 7;
Pred. No. 1.3e-163;
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                                                                                                                      Query Match
24.7%;
Best Local Similarity 99.6%;
Matches 1204; Conservative
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ive 0; Mismatches 4;
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bacherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter cell or pay prokaryotic RNA polymerases; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and courth recombination sites; (iii) 3' transcription terminating and fourth recombination sites, or the second and third recombination sites are identical. The first and second recombination sites, and preferably are identical. The first and second recombination sites, or the third and court recombination sites, do not recombination sites, or the third and same recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silending target nucleic acid sequences. The vectors can also be used to convert a DNA fragment and second also be used to convert a DNA fragment and second and second recombination sites.
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                                                  TGTCAACTGTCATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.
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Pred. No. 8.5e-160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ82143 standard; DNA; 17681
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29-NOV-2001; 2001US-0333743P.
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59.5%;
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3 CGCT(SCTTCATAGCACACTCTTTTTGACATACTTCGGGTAGTGCCGATCAACGTC 1
	TITICGCCAAAAGIIGGCCCAGGGCIICCCGGIAICAACAGGGACACCAGGAITTAI 1308
	TTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAAGTGCGTCGGGTGA 1368
FI FI	т -
<u>v</u> — v	araigitgigitttacagtattatgragicigittittatgcaaarictaattaa 1
8-8	GGIATTTATATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGTTGGCAT 154
AT 59	GGTCACTATCAGTCAAATAA 1
AATC CCCT	rrcggraccccagcrrgg 16
PAG GA	AAATAATTATTTTTTTTTTTTTAGTATAAAATAGTTAAGTGATGA
TAT 	RATAATATAGTIGTTATAATIGGAAAAATAATTIATAAATATTGTT 17:
TACA	TAPACAACATAGTAATGTAAAAAATATGACAAGTGATGTGTAAGACGAAGAAGAT 1
4 ≥ 2 ≥ 4	HAGTATATTATTAATGAATTTGATCGAACATGTAAGATGATATA 1900
CTAG	SCATTAADATTTGTTTTAATCATAATAGTAATTCTAGCTGGTTTGATGAATTAAATA 196.
% = %	aataaattaaaataat 203 getttgttacattaga 150
ATTI TTAC	TRATGATTAATAGTITATTATATAAATTAAATATCTATACCATTACTAAATATTT 2
AGT 	TTGTAATTTATCAATA 2
S F	-TATCAAACTAATAGAAAC 2
GTP.	AATCTAATGTAACAAAACATAATCTAATATATAACAAAGCGCAAGATCTATCA 224

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13697 TGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAAGAAGTGGCTGATC 13638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAGTATAAAGAGTTGTGAAATTGTTCTTGATGCAGATGATTTTCAGGACTATGACACT
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                                                                                                                                                                                                                                                                                                                                                                       13517 TIATCACGITTAGTAAGTATAGAGGCTGAAAATCCAGATGAAGCCGAACGACTTGTAAGA
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                                                                                    CGGGCGACCTCAGCCATCCCTGATTTTCCGCTTTCCAGCGTTC---GGCACGCAGA
                                                                                                                                                                                                                                                          rércadecrecerraracaceagecagererdeageregaracagaaarracagaaacr
                                                                                                                                                                                                                                                                                                                   ATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAG
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ABQ82141 standard; DNA; 17476
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2001US-0333743P.
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29-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>AATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGCTGAACGAGAAACGTAAAATGATA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGA
         TITIATATAGTATTATTTTCAATCAACATTCTTATTAAT-TTCTAAATAATACTTGTAGT
                                                                                                                        TITATIAACTICTAAATGGATIGACTATTAATTAAATGAATTAGTCGAACATGAATAAAC
                                                                                                                                                                                                                                     <u>racarcricaarcaaarrcarraaaaaraararacerracricaacritrarcricricci</u>
                                                                                                                                                                                                                                                                                                                                                        AGTTGGGAAGCTGGGTTCGAAATCGATAAGCTTGGATCCTCTAGAGAGCTGCAGCTGGAT
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Helliwell

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-WPI; 2002-682669/73

Claim 15; Page 74-83; 104pp; English

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising; (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and polyadenylation sites; (iii) 3' transcription terminating and polyadenylation sites, or the second and third recombination sites or the second recombination sites and fourth recombination sites, or the second recombination sites or identical. The first and second recombination sites, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide from the present invention seguence

Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

22.4%; Score 1089.4; DB 6; Length 17476; 59.4%; Pred. No. 1.2e-147; Indels Pred. No. 1.2e-147; 0; Mismatches 1336; Conservative st_Local Similarity tches 2314; Conserv 122 Query Match

16520 16340 ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAGAAGTATGTC 16280 16279 AAAAAGAGGTGTGCTATGAA---GCAGCGTATTACAGTGACAGTTGACAGCGACAGCTAT 16223 16640 16460 241 301 361 421 481 541 TCTTAIACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 601 GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATATTT 16639 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACAGACATATCCAGTC ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAAA TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA Acegaarcercerateraceceraceceratereceeraneeceratearareara 16399 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAAATAAAAAACATCTACCT ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC <u>AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATTTCCAGTC</u> 542 362 482 16459 422 242 16579 302 182 66991 a à d Dp à g δ g δ g ò qq ò à

15401 16163 15872 15871 GATGAAAGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGG 15812 15461 1428 1488 1548 15283 -CGAACCCAGCTTCCCAA- 15242 16051 ACTGGTGAAATGCAGTTTAAGGTTTACACCTATAAAAGAGAGGCGGTTATCGTCTGTTT 15992 -----CCAGTCTGCAGGT 15701 15640 adargangcoganggactrorangagagaagaagtarahangagirorgangcogargang 15581 1133 ATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATA 1192 901 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 781 recreccaacitagiceaciacaecraciaariaccarciaagiaeridaricalagiea TATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAAGTTGGCAT TATAAGAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAA <u> AATCATTATTTGCCATCCAGCTGCAGCTCCTCGAGGAATTCGGTACCCCCAGCTTGGTAAG</u> 1669 GAAATAATTATTTTTTTTTTCCTTTTAGTATAAATAGTTAAGTGATGTTAATTAGTAT --AGTCCCTGTTCTCGTCAGCAAAAGAGCC 1249 TCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACAGGGACACCCAGGATTTAT 15580 TCATTTTCGCCAAAAGTTGGCCCCAGGCTTCCCGGTATCAACAGGGACACCAGGATTTAT TTATTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAAGTGCGTCGGGTGA TTATTCTGCGAAGTGATCTTCCGTCACAGGTATTTATTCGGCGCAAAGTGCGTCGGGTGA TGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGA CTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAA 5340 TATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTACAAGTGGTC--CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA CAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAACCATGCAGA AGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT ATGAAGCCCGTCGTCTGCGTGCC---GAACGCTGGAAAGCGGGAAAATCAGGAAGGGATGG GTGGATGTACAGAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCCTGGCC 902 GIGICAAIAAIAICACICIGIACAICCACAAACAGACGAIAACGGCICICITITIAIAG 15931 AGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGCATATCGGG GIICATITCAATAAACCGGGGGGACCTCAGCCATCCCTTCCTGATTTTCCGCTTTCCAGCG GAAGAAGTGGCTGATCTCAGCCACGCGAAAATGACATCAAAAACGCCATTAACCTGATG ---GGCACGCAGGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGAT -CCGATCAACGTC crecararcricrerritacagrarrargragrererritrargcaaarcraarraa GAGACTTTATCTGACAGCAGAGGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGGC CTGAGGTCGCCCGGTTTATTGAATGAACGGCTCTTTTGCTGACGAGAACAGGG-1193 GGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTAGTG-15751 Trcrggggaararaargrcaggcrcccrraracacag GIGIAAACCIIAAACIGCAIITICACC----TAGAGGATCCAAGCTTATCGATTT 1309 1369 1429 1076 15520 15460 15400 1489 1549 1609 662 1016 602 722 16105 782 842 962 15811 16222 16162 15991 g g οp δ d $\dot{\delta}$ g ð d à

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STRANDEDNESS: double
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Sequence 22, Appl
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                                                                                                                                  Sequence 1, A
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Sequence 1, A
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Sequence 2, A
Sequence 3, A
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                                                                     May 8, 2004, 10:39:35 ; Search time 210.004 Seconds
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(GGTZ 6/ptodata2/ina/5A_COMB.seq:*
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-225-125A-2

US-09-225-152A-3

US-09-225-152A-3

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US-09-560-98B-78

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US-09-560-98B-78

US-09-560-98B-78

US-09-560-98B-1

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US-08-232-1016-22

US-08-064-101-11

US-08-478-015-11

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US-08-08-1899-11

US-08-351-413-2

US-09-577-424-3

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                                                                                                                                                                                   682709 seqs, 277475446 residues
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Listing first 45 summaries
                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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4340 TIGACAGTGACGACAAAATCGTTGGGGGGGGTCCAGGGGGGAATTTTGCGACAACATGTCGAG 4399
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4040 GGTCAAACCTAAAAGGCTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGC 4099
                                                                                                                                     4100 TAGTATCTACGACACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGTTC 4159
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APPLICANT: CORNELISSEN, Marc
APPLICANT: CORNELISSEN, Marc
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: DOCKX, Jan
APPLICANT: PLANT CELLS
ITILE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STRATE: Virginia
STATE: Virginia
COUNTRY: United States
ZIP: Z2313-1404
CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: McGowan, Malcolm K
REGISTRATION NUMBER: P39,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4792 GCTCAGCAGGACCTGCAGGCATGC 4815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/08232016 Patent No. 5952547
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 7639 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-232-016-22
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                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 3582.4407

TOTHER INFORMATION: /note= "3' regulatory sequence OTHER INFORMATION: containing the polyademylation site derived from Agrobacteriu OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                     /note= "Coding region of a truncated modified bt2 (crylAb) gene, also designated as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature

10CATION: 7071...7566

10CATION: 7071...7566

10THER INFORMATION: /note= "TR1' and TR2 promoter

10THER INFORMATION: derived from Agrobacterium T-DNA (with modified leader with

10THER INFORMATION: respect to sequence of pJD884 of SEQ ID NO. 22."

US-08-232-016-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3740 GATATTGCTTTCAATTCTGTTGTGCACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGA 3799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4072 GATCCATGCTAGCTCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCAT
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LOCATION: 2922..3581
OCHER INPORMATION: /note= "Coding sequence of
OTHER INFORMATION: ohloramphenicol acetyl transferase gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 2396.2921
OTHER INFORMATION: \note= "35S promoter sequence
OTHER INFORMATION: \derived from Cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to
as pPS0212
plasmid DNA designated
                                                                                                                                                                                                              crylAb6 gene."
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Best Local Similarity 98.8
Matches 735; Conservative
                                                                                                   LOCATION: 1..1785
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: FEATURE:
ORGANISM:
FEATURE:
                                                                        NAME/KEY:
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4491
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                                                 4124 GGTCAAACCTAAAAGAACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGGC
                                                                                                                                                                                         4184 TAGTATCTACGACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGTTC
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4432 GGTCAAACCTAAAAGACTGATTACATAAATCTTATTCAAATTTTCAAAAGGCCCCCAGGGGC
                                                                                                                                   4492 TAGTATCTACGACACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGTTC
                                                                                                                                                                                                                                                                    COCGCCGGCGCGATGGGTGAGTTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGA
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CONTENTAL ADDRESS:
CONTENT George Mason Bldg., Mashington & Prince Sts.
CITY: Alexandria
STATE: George Mason Bldg., Mashington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIR: 2213-1404
COMPUTER: EDAPH COMPATIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: 24-MAY-1993
CLASSIFICATION NUMBER: BP 90403332.1
FILING DATE: 23-NOV-1990
PRICH DATE: 23-NOV-1990
PRICH DATE: 23-NOV-1991
ATTORNEY AGENT INFORMATION FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON FATON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08064121
Patent No. 5641664
GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Crane-Peury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 5399 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-064-121-1
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NAME/KEY: misc_feature
LOCATION: 3666..4491
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
                                                                                                                                                                                                                                                  LOCATION: 1..1869
OTHER INFORMATION: /note= "Coding region of a
OTHER INFORMATION: truncated bt2 (cryIAb) gene, also designated as the bt884 gen
                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1877...2110
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4004 AAAATGAAAACAATATTGTGCTGAATAGGTTTATAGCGACATCTATGATAGAGCGCCA 4063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3824 GATATTTGCTTTCAATTCTGTTGTGCACGTTGTAAAAACCTGAGCATGTGTAGCTCAGA 3883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4192 TCCTTACCGCCGGTTTCGGTTCTAATGAATATATATCACCCGTTACTATCGTATTTTT 4251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4132 GATATTTGCTTTCAATTCTGTTGTGCACGTTGTAAAAAACCTGAGCATGTGGTAGCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4072 GATCCATGCTAGCTCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 3006..3665
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 2480..3005
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAWE/KEY: misc_feature;
1.OCATION: 7155..7639
1.OTHER INFORMATION: /note= "TR1' and TR2' promoter
1.OTHER INFORMATION: derived from Agrobacterium T-DNA."
US-08-232-016-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 5684..6541
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-la
                                                                                                                                              ORGANISM: plasmid DNA designated as pJD884
                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: 1877. 2110
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Matches 735; Conservative
                                                                                                                                                                                  FEATURE:
NAME/KEY: CDS
                                                                                                              ORIGINAL SOURCE:
              STRANDEDNESS:
TOPOLOGY: cii
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4573 GATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAAC 4632
                                  CCGGTCCAGCACGGCCGGGCAAACCGACTTGCTGCCCCGAGAATTATGCAGCATTTTT
                                                                                                                                                                                                                                                                                               2873 Trecretareresecceaaareaagrecaegreaaacerreacagreacea
                                                                                                                                                                                                                                          TTGGTGTATGTGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACGACAAATCGT
                                                                                                                      4633 CCGGTCCAGCACGGCCGGGTAACCGACTTGCTGCCCCGAGAATTATGCAGCATTTT
                                                                                                                                                                                                                                                                                                                                                                                                               2933 Tedecedercadecedarrrrecedecarateredadecreadedece
                                                                                                                                                                                                                                                                                                                                                             TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT
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SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,015
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: BP 91401888.2
APPLICATION NUMBER: BP 91401888.2
FILING DATE: 08-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,121
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INPORMATION:
NUMBE: MCGOWAN, MAICOLM NUMBER: MAICOLM NUMBER: US 08/064,121
ATTORNEY/AGENT INPORMATION:
NUMBE: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCGOWAN, MAICOLM NUMBER: MCG
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APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08478015; Patent No. 5712135; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
ORGANISM: plasmid pDE108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5399 base pairs
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STRANDEDNESS: double
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COUNTRY: United
ZIP: 22313-1404
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HYPOTHETICAL: N
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LOCATION:
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US-08-478-015-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2573 TATTATTACAAATCCAATTTTAAAAAGCGGCAGAACCGGTCAAAACCTAAAAGACTGAT 2632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2273 ccngcriraargagarargcgagacdccrargarcgcargararrrgcriricaarrcrgr 2332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2633 TACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGACACACCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATTATTACAAATCCAATTTTAAAAAAGCGGCAGAACCGGTCAAACCTTAAAAGACTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4093 CCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTTCAATTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRATURE:
NAME/KEY:
10CATION: 2101.3160
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: plyadenylation site derived from the OTHER INFORMATION: polyadenylation site derived from the OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= 35S3
/note= "35S3 promoter sequence derived from
Cauliflower mosaic virus isolate CabbB-JI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 99.7%; Pred. No. 6e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: -
LOCATION: 1285..2100
OTHER INFORMATION: /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycine OTHER INFORMATION: phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                      /label= pUC18
/note= "pUC18 derived sequence"
                                                 MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                     ORGANISM: plasmid pDE108 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                            452..1284
                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: - 452..1284
LOCATION: 452..1284
OTHER INFORMATION:
OTHER INFORMATION:
                        circular
                                                                                                                                                                                                                                                      LOCATION: 1..451
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: -
                                                                                                                                                                                                                                NAME/KEY:
                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-064-121-1
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2873 ITGGIGTATGTGGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACGACAAATGGT 2932
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OTHER INFORMATION: /note= "35S3 promoter sequence derived from
OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-JI"
                                                                                          2933 İGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGGCT
                                                  4753 TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCES: 5
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
CITY: Alexandria
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
APPLICANT: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,975
FILING DATE: 07-JUN-1995
CLASSIFCATION NUMBER: US 08/064,121
RIGHASHICATION NUMBER: US 08/064,121
APPLICATION NUMBER: US 08/064,121
FILING DATE: 23-NOV-1993
APPLICATION NUMBER: EP 94403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
APPLICATION NUMBER: EP 91401888.2
APPLICATION NUMBER: BP 91401888.2
ATTORNEY/AGENT INFORMATION:
NAME: CARACTERICATION:
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
TELECOMMULICATION INFORMATION:
TELEPHONE: (703) 836-2620
TELEPAX: (703) 836-2620
TELEPAX: (703) 836-2620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 US-08-475-975-1
; Sequence 1, Application US/08475975
; Patent No. 6002070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5399 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 452..1284
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OTHER INFORMATION:
OTHER INFORMATION:
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ORIGINAL SOURCE
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NAME/KEY:
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COTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
OTHER INFORMATION: site derived from the Agrobacterium T-DNA octopine synthase
OTHER INFORMATION: gene"
                                                                                                                                  /label= 35S3
/note= "35S3 promoter sequence derived from Cauliflower mosai
virus isolate CabbB-JI"
                                                                                                                                                                                                                                                        LOCATION: 1285..2100
OTHER INFORMATION: /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycine phosphotransferase gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
14.6%; Score 709.8; DB 1; Length 5399;
Best Local Similarity 99.7%; Pred. No. 6e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
               /label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                            2101..3160
                                                                                                                                                                                                                                      1285..2100
                                                                                                      LOCATION: 452..1284
CTHER INFORMATION: /
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FEATURE:
NAME/KEY:
                                                                                                              452..1284
                 OTHER INFORMATION: OTHER INFORMATION:
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NAME/KEY:
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FEATURE:
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                                                                                                                       /label= 3'ocs
/note= "3' regulatory sequence containing the
/note= "3' regulation site derived from the
Agrobacterium T-DNA octopine synthase gene"
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/label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                                                                                                                                                                                                                    OCCTION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.7
Matches 711; Conservative
                                                                                           NAME/KEX: 2101..3160
LOCATION: 2101..3160
OTHER INFORMATION: /la
OTHER INFORMATION: /nc
OTHER INFORMATION: pol
OTHER INFORMATION: ABI
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                    NAME/KEY:
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NAME/KEY:
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RESULT 6 US-09-084-889-1 ; Sequence 1, Application US/09084889

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FEATURE:

NAME/KEY: - 101..3160

OTHER INFORMATION: /label= 3'ccs
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
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OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from OTHER INFORMATION: Cauliflower mosaic virus isolate Cabbb-JI"
NAME/KEY: -
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STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
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/note= "pUC18 derived sequence"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TRY PC compatible
OPERATING SYSTEM
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/084,889
GENERAL INFORMATION:
APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, Elke
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,113
REPERENCE/DOCKET NUMBER: 010830-043
TELECOMMUNICATION: INFORMATION:
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APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-UL-1991
ATTORNEY/AGENT INFORMATION:
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PARIOR APPLICATION DATA:
APPLICATION UNMBER: 08/064,121
FILING DATE:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
ORGANISM: plasmid pDE108
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TYPE: nucleic acid
STRANDEDNESS: double
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COUNTRY: United States
ZIP: 22313-1404
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LOCATION: 1..451
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY:
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MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
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PRATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS:
TOPOLOGY: circ
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HYPOTHETICAL: N
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                                                                                                                                                                                                                   0;
                                                                                                                                                 Query Match
Best Local Similarity 99.7%; Pred. No. 6e-136;
Matches 711; Conservative 0; Mismatches 2; Indels 0;
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Patent No. 5750867
GENERAL INFORMATION:
APPLICANT: Williams, Mark
APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
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STATE: Vi
COUNTRY:
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US-09-084~889-1
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/label= 3'nos
/note= "3' regulatory sequence containing the
polyadenylation site derived from Agrobacterium
7-DAA nopaline synthase gene"
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OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from OTHER INFORMATION: cauliflower mosaic virus isolate Cabbb-JI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: complement (752..1024)
OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar gene
OTHER INFORMATION: Bacillus amyloliquefaciens"
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LOCATION: complement (1025..1607)

LOCATION: /label= TA29

OTHER INFORMATION: /note= "promoter derived from the TA29

OTHER INFORMATION: Nicotiana tabacum"

NAME/KEY:
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NAME/KEY: 241..3256
LOCATION: 241..3256
OTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
FOTHER INFORMATION: phosphotransferase gene of Tn5"
NAME/KEY: -
ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-TOS
OPERATING SYSTEM: PC-DOS/MS-TOS
OPERATING SYSTEM: PC-DOS/MS-TOS
OPERATING SYSTEM: PC-DOS/MS-TOS
OPERATING SYSTEM: PC-DOS/MS-TOS
OPERATING SYSTEM: PT-TOS (EPO)
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/note= "pUC18 derived sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,072
PILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
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complement (397..751)
RMATION: /label= 3'ros
RMATION: /note= "3' regulatory sequence containing the
RMATION: polyadenylation site derived from Agrobacterium
RMATION: T-DNA nopaline synthase gene"
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RMATION: /label= TA29
RMATION: /ne= "promoter derived from the TA29 gene of RMATION: Nicotiana tabacum"
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LOCATION: 1608..2440
OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from
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OTHER INFORMATION: /label= barstar
OTHER INFORMATION: /note= "coding region of the barstar or THER INFORMATION: Bacillus amyloliquefaciens"
FBATURE:
NAME/KEY:
                                                                                                                                      ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISC COMPUTIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
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/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: plasmid pVE144 (replicable in E.coli)
            CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 Bast STREET: 811s Church STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:

APPLICATION NUMBER: US 07/899,072

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/970,849

FILING DATE: 03-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30,330

REFERENCE/DOCKET NUMBER: 2121-102PCT

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX. 249345
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 205-8000 TELEFAX: (703) 205-8050
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OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: F
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OTHER INFORMATION: /
OTHER INFORMATION: /
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SEQUENCES:
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LOCATION: 1..396
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    LOCATION: 3257..4315
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /label= 3' ocs
OTHER INFORMATION: /label= 3' ocs
OTHER INFORMATION: /label= 3' ocs
OTHER INFORMATION: /label= 3' ocs
OTHER INFORMATION: T-DNA octopine synthase gene"
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                            TGTGCACGTTGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGTT
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APPLICANT: Leemans, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                              LOCATION: 4316..6555
COTHER INFORMATION: /label= puc18
OTHER INFORMATION: /note= "puc18 derived sequence"
US-08-351-413-
                                                                                                                                                                                                                                              Score 709.8; DB 1;
Pred. No. 6.4e-136;
0; Mismatches 2;
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Patent No. 5977433
GENERAL INFORMATION:
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.7%;
Matches 711; Conservative
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US-09-025-583-2
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Best Local S:
Matches 711
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OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-JI"

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| IOCATION: 4316..6555 |
| OTHER INFORMATION: /label= pUC18 |
| OTHER INFORMATION: /note= "pUC18 derived sequence" |
| US-09-025-583-2
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Pred. No. 6.4e-136;
0; Mismatches 2;
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Best Local Similarity 99.7%;
Matches 711; Conservative
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MGG-09-577-424-3
; Sequence 3, Application US/09577424
; Patent No. 6525245
; Patent No. 6525245
; GENERAL INFORMATION:
APPLICANT: Rhoads, David M
; TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
; TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
; CURRENT APPLICATION NUMBER: US/09/577,424
; CURRENT FILING DATE: 200-05-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.6%; Score 709.8; DB 4; 99.7%; Pred. No. 8e-136; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
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                                                                                                                                                                                                                                                                            11941 TGGTGTATATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACGACAAATGGT
12061 ATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAACC
                                                                                                                                                      12001 GGGTCCAGCACGGCCGGGGAACCGACTTGCTGCCCCGAGAATTATGCAGCATTTTT
                                                                                                                                                                                                                        TGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACGACAAATCGTT
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                                                                                                                                                                                                                                                                                                                                                 4754 GGGCGGGTCCAGGGCGAAITITIGCGACAACAIGICGAGGCTCAGCAG 4800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bedbrook, John R.
APPLICANT: Dunsmul: Pamela
APPLICANT: Howis, William J.
APPLICANT: Joe, Lawrence K.
APPLICANT: Lee, Kathleen Y.
APPLICANT: NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 941113834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING YSTERM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 566.4; DB 2;
99.8%; Pred. No. 1.7e-106;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    012176-005010US
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APPLICATION NUMBER: US/08/673,768
FILING DATE: 27-UTN-1996
CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-UTN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L.
REGISTRATION UNUBER: 34,774
REFRENCHOCKET NUMBER: 0121
TELECOMMUNICATION INFORMATION:
TELEFAM: (415) 576-0200
INPORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08673768
Patent No. 5952546
GENERAL INFORMATION:
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Dunsmuir, Pamela
Howie, William J.
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nucleic acid
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Best Local Similarity 99.8
Matches 567; Conservative
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TOPOLOGY: lin
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US-08-673-768-1
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Pred. No. 3.5e-135;
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                                                                                                               APPLICANT: BARKER, RICHARD F.;KEMP, JOHN D.
APPLICANT: BARKER, RICHARD F.;KEMP, JOHN D.
TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/91,538
FILING DATE: 13-ADR-1992
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 869,216
FILING DATE: 1-NOV-1989
APPLICATION NUMBER: 553,786
FILING DATE: 19-NOV-1989
APPLICATION NUMBER: 553,786
FILING DATE: 0-NOV-1983
APPLICATION NUMBER: 141,775
FILING DATE: 0-NOV-1983
APPLICATION NUMBER: 144,775
FILING DATE: 0-NOV-1983
APPLICATION NUMBER: 13,624
FILING DATE: 1-NOV-1983
APPLICATION NUMBER: 13,624
FILING DATE: 1-NOV-1983
APPLICATION NUMBER: 13,624
FILING DATE: 1-NOV-1983
APPLICATION NUMBER: 260,574
FILING DATE: 1-O-JUN-1931
APPLICATION NUMBER: 260,574
FILING DATE: 1-O-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%; Sco. 100.0%; Pred. No. ... 0; Mismatches
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FILING DATE: 26-SEP-1983
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Best Local Similarity
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5428147-1
                                                                                                        5428147
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                                             RESULT 10
5428147-1/c
                                                                                                        Patent No.
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13914 GATTÓCTTGAAGTTGAGTATTGGCCGTCTGCTACCGAAAGTTACGGCACCATTCAAC 13855
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Patent No. 5910438
GENERAL INFORMATION:
APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   11.6%; Score 566.4; DB 2; 99.8%; Pred. No. 1.7e-106; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CIIY: Newport Beach
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                   SEQUENCE CHARACTERISTICS:
LENGTH: 15397 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                       Query Match
Best Local Similarity 99.8
Matches 567; Conservative
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MEDIUM TYPE: Diskette
INFORMATION FOR SEQ ID NO:
                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
                                                                                                            TOPOLOGY: 11 MOLECULE TYPE:
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COUNTRY:
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                                                                                                                                                                               7290 ATTTACTGATTGTACCCTACTTATATGTACAATATTAAAATGAAAACAATATATTGT 7349
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                                                                                           7230 CATTCTAATGAATATATCACCCGTTACTATGGTATTTTTTATGAATAATATTCTCCGTTCA
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  7170 IGTGCACGITGTAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTTCGGTT
                                                                                                                                         ATTTACTGATTGTACCCTACTTATATATGTACAATATTAAAATGAAAACAATATATTGT
                                                                                                                                                                                                                             TITLE OF INVENTION: Delayed Ripening Tomato Plants
WAMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,768
FILING DATE: 27-JUN-1996
CLASSIFICATION: 800
CLASSIFICATION BATA:
APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 012176-005010US
TELECHOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4633 CCGGTCCAGCACGCCGCCGGTAACCG 4660
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Patent No. 5952546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bachrock, John R.
APPLICANT: DUNSMULY, Pamela
APPLICANT: Howie, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Joe, Lawrence K.
Lee, Kathleen Y.
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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California
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US-08-673-768-1/c
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APPLICANT:
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Fatent No. 5910438
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bernard, Philippe
APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
APPLICANT: Gabant, Philippe
APPLICANT: Gabant, Philippe
APPLICANT: Gabant, Philippe
APPLICANT: Gabant, Philippe
CORRESPONDENCE: 6
CORRESPONDENCE: 6
CORRESPONDENCE: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                         Query Match 6.7%; Score 325.4; DB 3; Best Local Similarity 99.7%; Pred. No. 1.1e-57; Matches 326; Conservative 0; Mismatches 1;
                                                                                 NUMBER OF SEQ ID NOS: 10
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 420
CURRENT APPLICATION NUMBER: US/09/225,152A CURRENT FILING DATE: 1998-01-04 PRIOR APPLICATION NUMBER: 08/379614 PRIOR FILING DATE: 1995-07-20
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,614
                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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CLASSIFICATION: 435
PRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 02-AUG-1993
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US-08-379-614-3/c
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US-09-225-152A-2/C
US-09-225-152A-2/C
; Sequence 2, Application US/09225152A
; Patent No. 6180407
; GENERAL INFORMATION:
; APPLICANT: Bernard, Philippe
; TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
; FILE REFERENCE: VANMAIO.001CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 325.4; DB 2
Pred. No. 1.1e-57;
0; Mismatches 1
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                                                                                                                                                                                                                                                            VANMA10.001APC
                                                            rrrraraggreraaaccrraaacreca 77
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OPERATING SYSTEM: DOS
SOSTWARE: FRSESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.7%;
Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 1...378
; OTHER INFORMATION:
US-08-379-614-2
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MOLECULE TYPE: Ge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 GIGTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGAT
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                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 base pairs
TUPDCTH: 416 base pairs
TVPE: nucleic acid
STRANDEDNESS: single
TOPDCLOGY: both
WOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
HYPOTHETICAL: NO
RANI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: ccd8 gene of plasmid pKIL 19
ATTORNEY/AGENT INFORMATION:
NAME: Alteman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMAIO.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0604
TELEFAX: 714-760-9502
TELEFAX: 714-760-9502
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LCCATION: 1...378
CTHER INFORMATION:
US-08-379-614-3
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Search completed: May 9, 2004, 22:12:59 Job time : 213.004 secs Н

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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/CT_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_PUBGOMB.seq:*
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version 5.1.6
- 2004 Compugen Ltd.
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15 US-10-055-001A-24 Sequence 24, Appl 15 US-10-055-01A-25 Sequence 25, Appl 15 US-10-055-01A-25 Sequence 25, Appl 15 US-10-055-01A-13 Sequence 3, Appl 15 US-10-44-3315-3 Sequence 3, Appl 15 US-10-44-3315-3 Sequence 3, Appl 15 US-10-353-454-31 Sequence 3, Appl 15 US-10-353-454-57 Sequence 37, Appl 15 US-10-353-454-57 Sequence 37, Appl 16 US-10-353-454-31 Sequence 31, Appl 16 US-10-353-454-31 Sequence 31, Appl 16 US-10-353-454-31 Sequence 31, Appl 16 US-10-17-478-20 Sequence 21, Appl 17 US-10-17-48-20 Sequence 31, Appl 17 US-10-17-48-20 Sequence 20, Appl 17 US-10-17-48-20 Sequence 20, Appl 17 US-10-17-48-20 Sequence 20, Appl 17 US-10-151-690-20 Sequence 27, Appl 17 US-10-151-690-20 Sequence 27, Appl 17 US-10-151-690-21 Sequence 21, Appl 17 US-10-151-690-21 Sequence 21, Appl 18 US-10-151-690-21 Sequence 21, Appl 18 US-10-151-690-21 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 18 US-10-151-690-61 Sequence 21, Appl 21 US-10-151-690-61 Sequence 21, Appl 21 US-10-151-690-61 Sequence 21, Appl 21 US-10-151-690-61 Sequence 21, Appl 21 US-10-151-690-61 Sequence 21, Appl 21 US-10-151-690-61 Sequence 21, Appl 21 US-10-151-690-61 Sequence 21, Appl 25-11 Sequence 21, Appl 21 US-10-162-214-4	ESULT 1 IS-10-055-001A-23 Sequence 23, Application US/1005501A Sequence 23, Application US/1005501A Sequence 23, Application US/1005501A Sequence 23, Application US/1005501A Sequence 23, Application US/1005501A APPLICANT: Waterhouse, Petepher A. APPLICANT: Waterhouse, Petepher A. TITLE OF INVENTION: Wathod and means for producing efficient silencing constructs TITLE OF INVENTION: using recombinational cloning FILE REFERENCE: HELLGA CURRENT APPLICATION NUMBER: US/10/055,001A CURRENT APPLICATION NUMBER: US/10/055,001A CURRENT FILING DATE: 2002-06-11 SEQ ID NO 23 LENGTH: 17862 TYPE: DNA SEQ ID NO 23 LENGTH: 17862 TYPE: DNA SEQUENCE: Artificial sequence FEATURE: OTHER INFORMATION: acceptor vector pHELLSGATE4 IS-10-055-001A-23	0%; Score 4863; DB 15; Length 17862; 0%; Pred. No. 0; 0; Mismatches 0; Indels 0; Gaps	TITCALTIGGAGAGGACACGCTCGAGGCTAGCATCTCGGGCCCCAAATAATGATTT 60	TATTITGACTGATACTGACCTGITCGTIGCAACAAATIGATGAGCAATGCTTTTTATAA 120
22.4 17476 22.4 17476 17.3 11651 16.0 786 15.2 2016 15.2 2016 15.1 3034 15.1 3034 15.1 3034 15.1 3034 15.1 3034 16.2 2867 16.3 2867 17.3 304 17.3 2067 17.3 2067 17.3 2067 17.3 2067 17.3 2067 17.3 2067 17.3 2067 17.3 2067 17.4 5286 17.4 627 10.1 4627 10.1 4627 10.1 4627 10.1 4627 10.1 4627 10.1 4627 10.1 4627	LIT 1 055-001A-23 quence 23, Application US/10055001A blication No. US/2030049835A1 NERAL INFORMATION: PPLICANT: Waceley, Susan V. PPLICANT: Waley, Susan V. PPLICANT: Walelyouse, Peter PPLICANT: Helliwell, Christopher A. ITLE OF INVENTION: Wethod and means ILE REPERENCE: HELLGA URRENT APPLICATION NUMBER: US/10/05 UNBERT FILING DATE: 2002-06-11 UNBERT FILING DATE: 2002-06-11 UNBERT FILING DATE: 2002-06-11 UNBERT FILING DATE: 2002-06-11 UND NO 23 TYPE: DNA O ID NO 23 TYPE: DNA FRATURE: COGGANISM: Artificial sequence PERTURE: OTHER INPORMATION: acceptor vector 0-055-001A-23	100 al Similarity 100 4863; Conservative	CATTTGGAGAGG 	tttgactgatag tttgactgatag
1100801 10080 1008	RESULT 1 US-10-055-001A-23 Sequence 23, Applica Publication No. US20 GENERAL INFORMATION: APPLICANT: Waterho, APPLICANT: Waterho, APPLICANT: Waterho, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TILLE OF INVENTION: TORGANIAM: ARLIFICI FEATURE: COTHER INFORMATION: US-10-055-001A-23	atch cal S 4863	1 TTT 1	61 TAT 13060 TAT
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16420 CCAGOCTICACACOACCACCACACACACACACACACACACACACACA
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231 TAMATGALTHGTCGAACHTGAATTAACAGGTAACATGATGATCATCATCATCATCTTGTTTA 15399 2411 TOATTGATCTTAACTTACATTGGAATTGATTACATGATGATCATCATCTAACT

13325 ASANTANGAMANAGOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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1750 CACACACCACCACCACCACCACCACACTACTACTACACCAC

1742 INCITIOTINIAATTOTGAAAAATATTITIAAATATTITIAATATTOTTAAAAAAAAA	2642 AAAAACAGACTACATAATACTGTAAAACACATATCCAGTCACTATGAATCAACTACT 2701 15360 AAAAACAGACTACATAATACTGTAAAACACATATCCAGTCACTATGAATCACTACT 2701 15360 AAAAACAGACTACATAATACTGTAAAACACATATCCAGTCACTATGAATCACTACT 15419 2702 TAGATGGTATTAGTGACCTGTAGTCGACTAGGTTGGCAGCATTTGCG 2761 15420 TAGATGGTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACCCGAGCACTTTGCG 15479 2762 CCGAATAAATACCTGTGACGGACTAAGTTGGCAGCACTCACCCGAGGCACTTTGCG 15479 15480 CCGAATAAATACCTGTGACGGAAGATCACTTGGCAGAATAAATCCTGGTGTCCCTG 2821 15480 CCGAATAAATACCTGTGACGGAAGATCACTTCGCAGAATAAATA
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ATATCALTITYACGITICTCGTTCAGCTTTCTTGTACAAAGTTGGCATTATAAGAAAGCAT 1561
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APPLICANT: Waterhouse, Peter APPLICANT: Waterhouse, Peter TITLE OF INVENTION: Method and means for producing efficient silencing of TITLE OF INVENTION: Wethod and means for producing efficient silencing TITLE OF INVENTION: using recombinational cloning FILE REFERENCE: HELLGR COURENT APPLICATION NUMBER: US/10/055,001A CURRENT FILING DATE: 2002-06-11 NUMBER OF SEQ ID NOS: 26 SOFTWARR: Patentin version 3.1 SEC ID NO 26 LENGTH: 17681
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Pred. No. 0;
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Matches 4477; Conservative
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Sequence 25, Application US/10055001A

Publication No. US20030049835A1

GENERAL INFORMATION:

APPLICANT: Wesley, Susan V.

APPLICANT: Wesley, Susan V.

APPLICANT: Helliwell, Christopher A.

TITLE OF INVENTION: Method and means for producing efficient silencing constructs

TITLE OF INVENTION: Using recombinational cloning

FILE REFERENCE: HELLGA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT PILING DATE: 2022-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 25

LENGIH: 17458

TYPE: DNA

ORGANISM: Artificial sequence
               RESULT 5
US-10-055-001A-25
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                                                                                                                    122 GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATATT
                                                                                                                                                                                    AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACAACATATCCAGTC
                                                                                                                                                                                                                                                   TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA
                                                                                       Gaps
                                                         Length 17458
                                                                                       308;
                                                                                       Indels
                                                                                         15.
                                                           DB 15;
     ; FEATURE:
; CTHER INFORMATION: acceptor vector pHELLSGATE11
18-10-055-001A-25
                                                         Score 4042; DB
Pred. No. 0;
0; Mismatches
                                                           Query Match
Best Local Similarity 93.2%;
Matches 4419; Conservative
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                                                                                                                           AGGAATAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAATAAAAACATCTACC
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                                                                     1300 AIGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCA
                                                                                                                                                                                                                                                   TATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAA
                                                                                                        361 AACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAA
                                                                                                                                                                             AAGAAATAAGAAAAAGAGGGGGGGCCTCTTTTTTGTGTGACAAAATAAAAACATCTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             terminator region
                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (16551)..(16319)
OTHER INFORMATION: attP2 recombination site (complement)
   OTHER INFORMATION: attP1 recombination site (complement)
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (13675)..(13980)
OTHER INFORMATION: ccdB selection marker (complement)
                                   NAME/KEY: misc feature
LOCATION: (17610)..(16855)
OTHER INFORMATION: ccdB selection marker (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (264)...(496)
LOCHER INFORMATION: nopaline synthase gene promoter
FEATURE:
                                                                                                                                                                                                                                                                     LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

LOCATION: (2149)..(2706)

/ THEN INFORMATION: a left T-DNA border region

US-10-055-001A-13
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Pred. No. 0;
0; Mismatches
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LOCATION: (13048)..(13279)
OTHER INFORMATION: attPl recombination site
FEATURE:
                                                                                                                                                                                                                                                                                                                                                             recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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ION: (497)..(1442)
INFORMATION: nptII coding region
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                                                                                                                                                                                                                   N
                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (14660)..(16258)
OTHER INFORMATION: pdk2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%;
ilarity 85.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine
                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (14387)..(14619)
OTHER INFORMATION: attp2 r
                                                                                                                                                                                                                                                   misc_feature (15002)..(150
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Best Local Similarity
Matches 4846; Conserv
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LOCATION:
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NAME/KEY:
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Sequence 23, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Sysan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Welly Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
FILE REFERENCE: HELLGA
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Pred. No. 6.9e-242;
0; Mismatches 1355;
                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: acceptor vector pHELLSGATE4
                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 23
                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                     Query Match 33.8%;
Best Local Similarity 65.2%;
Matches 2668; Conservative
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US-10-055-001A-23
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85 CGTTGCCACCAATTGATGAGCAATGCTTTTTATAATGCCAACTTTGTACCAAAAAGCTG 65 CGTTGCCACAATTGATGAGCAATGCTTTTTTTTATAATGCCAACTTTGTACAAAAAAGCTG 65 CGTTGCAACAATTGATGATAATGCTTTTTTTTTAATTGCACTTTTGTACAAAAAAGCTG 66 CGTTGCAACGTAAAATGATATAAATTAAATTAAATTGCATAAAAAA 67 AACGAGAAACGTAAAATGATAAAATATCAATATTAAATTAGATTTTGCATAAAAAA 68 AACGAGAAACGTAAAATGATAAATATATAAATTAGATTTTGCATAAAAAAA 69 AACGAGAAAACGTAAAATGATAAATTAAATTAAATTAGATTTTGCATAAAAAAA	QY 205 AGACTACATAATACTGTAAAACACAACAAATGTCACTACGATCAATACTTAGATG 264 DD 185 AGACTACATAATACTGTAAAACAACATATCCAGTCACTATGAATCAACTTTAGATG 244 QY 265 GTATTAGTGACCTGTAGTCGACCAACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAA 324 DD 245 GTATTAGTGACCTGTAGTCCAACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAA 304	325 CITAGICGACAGCCITCCAAAIGITCITCICAAACGGAAICGITGICGGCCTA	Db 365 CTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAAGAAAAAAGAAAAAAGGGGCGA 424 Qy 445 GCCTCTTTTTGTGTGACAAAATAAAACATCTACCTACTCATATACGCTAGTGTCATAG 504 Db 425 GCCTCTTTTTGTGTGACAAAAAAACATCTACCTACTATATACGCTAGTGTCATAG 484	Qy 505 TCCTGAAAATCATCTGCATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGT 564	Qy 565 CGTTCGGCTTCATCTGGCTCTATACTTACTAAAGGTGATAAAGTTTCTGTA 624	Qy 625 AITTCTACTGTACTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCC 684	Oy 685 CCAGAACATCAGGTTAATGGGGTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCAC 744	OY 745 ITCITCCCCGAIAACGGAGACGGCACTGGCCATAICGGTGGTCAICGCCAGCT 804	QY 805 TTCATCCCCGATATGCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCGGAGG 864 Db 785 TTCATCCCCGATATGCACCACGGGTAAAGTTCACGGGGAGACTTTATCTGACAGCAGGG 844	OY 865 IGCACTGGCCAGGGGATCACCATCCGTCGCCCGGGGGTGTCAATAATATCACTCTGTAC 924	OY 925 AICCACAAACAGACAAACAGCICICICITITATAGGIGTAAACCITAAACIGCAITIC 984	cctgitctcgtcagcaaaaggccgttcatttcaataaaccgggcgacttcag 	1045	DD 1085 GCATGGCTTACCAGAGGATATTGACATCATATATGCCTTGAGCAACTGATA 1144
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1165 GCTGTCGCTGTCAACTGTCATGTAATACGG 1225 CTTCGGGTA 1233 Db 1225 CTTCGGGTA 1233 Db 1225 CTTCGGGTA 1233 DG-10-357-268-1 Sequence 1, Application US/10357268 Publication No. US20030219902A1 APPLICANT: House, Brent L APPLICANT: House, Brent L APPLICANT: House, Brent L APPLICANT: House, Brent L APPLICANT: House, Brent L APPLICANT: House, Brent L APPLICANT: MONTHMER: US/10/357,268 CURRENT APPLICATION WHERE: US/10/357,268 CURRENT PILING DATE: 2003-01-31 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR PLING DATE: 2002-01-31 CURRENT FILING DATE: 2002-01-31 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR APPLICATION NUMBER: 60/354,063 PRIOR APPLICATION: 1200-01-31 FRATURE: NAME/KEY: terminator LOCATION: (223)(275) OTHER INFORMATION: T1 FRATURE: NAME/KEY: gene LOCATION: (332)(563) OTHER INFORMATION: CAGE GENE NAME/KEY: gene LOCATION: (332)(563) OTHER INFORMATION: ALTP1 recombination FRATURE: NAME/KEY: gene LOCATION: (2689)(3577) OTHER INFORMATION: ALTP2 recombination FRATURE: NAME/KEY: gene LOCATION: (2868)(3577) OTHER INFORMATION: ALTP2 NAME/KEY: gene LOCATION: (2859)(1264) OTHER INFORMATION: ALTP2 NAME/KEY: gene LOCATION: (2869)(3577) OTHER INFORMATION: ALTP3 PRATURE: NAME/KEY: gene LOCATION: (2869)(3577) OTHER INFORMATION: ALTP3 PRATURE: NAME/KEY: gene LOCATION: (2869)(3577) OTHER INFORMATION: ALTP3 PRATURE: NAME/KEY: gene LOCATION: (2869)(3577) OTHER INFORMATION: ALTP3 NAME/KEY: gene LOCATION: (2869)(3577) OTHER INFORMATION: ALTP3 PRATURE: NAME/KEY: gene LOCATION: (2869)(3577) OTHER INFORMATION: ALTP3 PRATURE: NAME/KEY: GENE LOCATION: (2869)(3577) OTHER INFORMATION: ALTP3 PRATURE: NAME/KEY: GENE LOCATION: (2860)(3577) OTHER INFORMATION: ALTP3 OTHER INFORMATION: ALTP3 OTHER INFORMATION: ALTP3 P		OY 145 AACGAGAAACGTAAAATGAT	Oy 205 AGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTATGAATCAACTAACT	Oy 265 GTATTAGTGACCTGTAGTCGACCGACAGCTTTCTAAATGTTCTTCGGGTGATGCTGCCAA 324	or facilitating Site-Specific Recombination Oy 325 CTTAGTCGACGACAGCCTTCCAAAGGTCTTCTCAAACGGAATCGTATCGTATCGTCTATAGCCTT Oy 305 CTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTATCGTATCGTATCGTATCCTAGCCTTA 3	385 QY 385 Db 365	OY 445 GCCTCTTTTTGTC OY 425 GCCTCTTTTTGTC Db 425 GCCTCTTTTTTGTC	Qy 505 TCCT Qy 1	QY S6S CGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTA 624 1020(275) Db 545 CGTTCGGCTTCATCTAGAATTTCAGCCTCTATACTTACTT	OY 625 ATTICTACTGTATCGACCTGCAGACTGGGACCTGACATTTATATTCC 684	P1 recombination site Db 665	OY 745 TICTICCCCGAIRACGGAGACCGGCACACTGGCCATAICGGTGGTCATCATGGCCAGCT 804		QY 865 TGCACTGGCCAGGGGGGATCACCATCGCTCGCCCGGGCGTGTCAATAATATCACTCTGTAC 924 1 1 1 1 1 1 1 1 1 1		985 ACCAGTCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAG 1044 965 ACCAGTCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAAACCGGGCGACCTCAG 1024 bb 965 ACCAGTCCTGTCAGCAAAAAAAACCGGGCGACCTTCATTCA	
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-61/c No. US2003 DRMATION: BRASCH, M CHEO, DAV LI, XIAO ESPOSITO, BYRD,	625 ATTICIACTORATICACCICCICALACIGGACCICCICALATATATATIC 684 4980 ATTICIACTORATICACCICCACACTGCACACTGCACACTATATATATIC 691 4920 CCACAACATTATACCCTTATACCCTTATACCCCCTCACATTATACACCCCCC
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US-10-151-690-63

Sequence 63, Application US/10151690

Publication No. US20030124555A1

Gequence 63, Application US/10151690

Publication No. US20030124555A1

APPLICANT: BRASCH, MICHAEL A.

APPLICANT: CHEO, DAVID

APPLICANT: LIXAO

APPLICANT: BYRD, DEVON R.N.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO

FILE REPERENCE: 0942.5120001

CURRENT APPLICATION NUMBER: US/10/151,690

FRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-21

FRIOR FILING DATE: 2001-05-21

FRIOR FILING DATE: 2001-05-31

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin version 3.1

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24.6%; Score 1194.6; DB 1:
Best Local Similarity 99.7%; Pred. No. 3.6e-173;
Matches 1197; Conservative 0; Mismatches 4;
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TYPE: DNA
ORGANISM: Artificial sequence
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US-10-151-690-62
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Best Local Similarity 99.6%;
Matches 1204; Conservative
SOFTWARE: Patentin version
EQ ID NO 62
LENGTH: 4428
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### APPLICANT: BRASCH, MICHAEL A. ### APPLICANT: CHEO. DAVID #### APPLICANT: CHEO. DAVID #### APPLICANT: CHEO. DAVID #### APPLICANT: CHEO. DAVID #### APPLICANT: CHEO. DAVID #### APPLICANT: CHEO. DAVINIC #### APPLICANT: BYRD, DEVON R.N. #### APPLICANT: BYRD, DEVON R.N. #### APPLICANT: BYRD, DEVON R.N. #### TILLE REFERENCE: 0942.5120001 #### CURRENT APPLICATION NUMBER: US/10/151,690 #### PRIOR PLILICATION NUMBER: US 10/151,690 #### PRIOR PLILICATION NUMBER: US 60/291,973 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 ### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILING DATE: 2001-05-21 #### PRIOR PLILICATION NUMBER: US 60/291,973 #### PRIOR PLILICATION NUMBER: US 60/291,973 #### PRIOR P	Ouery Match 24.6%; Score 1194.6; DB 15; Length 4627; Best Local Similarity 99.7%; Pred. No. 3.6e-173; Marches 1197; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	Oy 33 AIGGAICICGGGCCCCAAAIAAIGAITITATITIGACIGAIAGIGACCIGITCGIIGCAA 92	QY 93 CAAATTGATGAGCAATGCTTTTTATAATGCCAACTTTGTACAAAAAGCTGAACGAGAA 152 	OY 153 ACGTAAAATGATAATAATATGAATATTAAATTAGATTTTGCATAAAAAGGACTACA 212 	OY 213 TAATACTGTAAAACACATATCCAGTCACTATGAACTACTTAGATGGTATTAGT 272	QY 273 GACCTGTAGTGGACCACGACGACTTCCAAATGTTCTTGGGGTGATGCTGCCAACTTAGTCG 332	Qy 333 ACCGACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCTACTCGCTAT 392	OY 393 IGICCTCAATGCCGTATTAAATCATAAAAAGAAATAAGAAAAAGGGTGCGAGCCTCTT 452	OY 453 TITGIGIGACAAAAAAACAICTACCTATICATATACGCTAGIGICATAGICCIGAAA 512 	OY 513 ATCATCTGCATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGC 572	QY 573 TTCATCTGGATTTTCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAATTTCTAC 632	QY 633 TGTATCGACCTGCAGACTGGCTGTATAAGGAGCCTGACATTATATTCCCCAGAACA 692
273 GACCTGTAGTCGACCACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCG 332 241 GACCTGTAGTCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCCAACTTAGTCG 330 333 ACCGACAGCCTTCCAAATGTTCTTCTCAAATGTTCTTCGGGTGATCCTGCTATCGCTAT 392 301 ACCGACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCTACTGCTAT 360 393 TGTCCTCAATGCCTTTAAATCATAAAAAGGAATCGTCGTATCCAGCCTACTGCTAT 420 453 TTTGTGTGACAAATTAAATCATAAAAAGAAATAAAAAAAA	633 IGIALGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCAGAACA 692 	693 TCAGGITAAIGGCGITITIGAIGICAITITICGCGGIGGCTGAGAICAGCCACITCTICCC 752	753 CGATAACGGAGACGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCC 812 	813 CGATATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGAGGAGACGTGCACTGG 872 	873 CCAGGGGGATCACCATCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAA 932 	933 ACAGACGATAACGGCTCTCTTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCC 992	993 CTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCT 1052	1053 TCCTGATTTTCCGCTTTCCGCACGCACGCACACGACGGCCTTCATTCTGCATGGTT 1112 1021 TCCTGATTTTCCGCTTTCCAGCGTTCGGCACGACGACGGCTTCATTCTGCATGGTT 1080	1113 GIGCTIACCAGACCGGAGATATTGACATCATATGCCTTGAGCAACTGATAGCTGTCGC 1172 	1173 TGTCAACTGTCACTGTAATACGCTGCTTCATAGCACCTCTTTTTGACATACTTCGGGT 1232	1233 A 1233 1201 A 1201	SULT 13 -10-151-690-64 Sequence 64, Application US/10151690 Publication No. US20030124555A1

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661 TAGGTTAATGGGGTTTTTTGATGTTTTTGATGTTGATGGGGGG	CURRENT FILING DATE: 2002-06-11 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin version 3.1 SEQ ID NO 26 LENGHA: 17681 TYPE: DNA ORGANISM: Artificial sequence FEATURES: CORGANISM: Artificial sequence CHERT INFORMATION: acceptor vector pHELLSGATE12 ORGANISM: Artificial sequence CHERT INFORMATION: acceptor vector pHELLSGATE12 ORGANISM: Artificial sequence MACHER INFORMATION: acceptor vector pHELLSGATE12 CHERT INFORMATION: acceptor vector pHELLSGATE12 ORGANISM: Artificial sequence MACHER INFORMATION: acceptor vector pHELLSGATE12 ORGANISM: Acceptor vec

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2489	GGCAAATAATGATTTTTTGACTGATAGTGACCTGTTCGTTGCAACAAATTGATAAGC 2548
2549	AATGCTTTCTTATAATGCCAACTTTGTACAAGAAAGCTGAAGAGAAAGGTAAAATGATA 2608
2609	Taaatatcaatatataaattagattttgcataaaaacagactacataatactgtaaaa 2668
2669	CACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTGGG 2728
2729	CTAAGTIGGCAGCAICACCCGACGCACITIGCGCCCAAIAAATACCTGIGACGGAAGAIC 2788
2789	ACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAACT 2848
2849	TITGGCGAAAATGAGACGITGAICGCCACTACCCAITTCACAACTCTIAIACTITTCTCT 2908
2909	TACAAGTCGTTCGSCTTCATCTGGATTTTCAGCCTCTATACTTACTAAAGGTGATAAAGT 2968
2969	TTCTGTAATTTCTACTGTATCGACCTGCACACTGGCTGTGTATAAGGGAGCCTGACATTT 3028
3029	ATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATCATCTTTTCGCGGTGGCTGAGAT 3088
3089	CAGCCACTICTICC
3149	GCCAGCTITCATCCCCGATAIGCACCACCGGGTAAAGTICACGGGAGACTITATCTGACA 3208
3209	GCAGACGIGCACTGGCCAGGGGATCACCATCCGTCGCCCGGGGGGTGTCAATAATATCAC 3268
3269	TCTGTACATCCACAAACAGACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACT 3328 CAGATAAAGTCTCCCGTGAACTTTACCGGTGCATATCGGGGATGAAAGCTGGGGCA 13698
3329	GCATTTCACC-
3383	CGGGCGACCTCAGCCATCCTGATTTTCCGCTTTCCAGCGTTCGGCACGCAGA 3439

3440 CGACGGGCTTCATTCTGCATGG---TTGTGCTTACCAGACGGGAGATATTGACATCATAT 3496

16639 AANTTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTC 16580 242 ACTATGAATCAACTTAGATGGTATTAGTGACCTGTAGTCGACCGAC	ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAACACACAC	662 AGGAGCCTGACATTTATATTCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 721 16162 ATGAAGCCCTCGTCTGCTGTCTCGAACGCTGGAAAATCAGAAGGAAATT 721 16162 ATGAAGCCCTCGTCTGCTGCCGAACGCTGGAAAATCAGAAATCAGAAGGATGG 16106 722 TGGCGGGGGTGGTGATCATTCATCTGATGAAGGAGAACGGGAAAATCAGGCATA 781 16105 CTGAGGTGGTCGTTTATTGAAATGAACGGCTCTTTTGCTGACGAGAACAGGG 16052 782 TCGGTGGTCATCATGGCCCAGCTTTAAACATTCCCCGATATGCACCACGGGTAAAGGTCACGG 841 16051 ACTGGTGAAATGCAGTTTAAACATTAACCTTATAAAAAAAA	842 GAGACTTTATCTGACAGCAGACGTGCACTGGGCAGGGGGATCACCATCCGTCGCCCGGGC 901 15991 GTGGATGACAGCAGAGACGTGCACTGCCCGGGCG 15932 902 GTGTCAATAATATTATTATACACCCCGGGCGATGGTGATCCCCCTGGCC 15932 15931 AGTGCACTCTGTACATCATCCACAACAGACGATGATAACGGCTCTTTTTATAG 961 15931 AGTGCACGTCTGTTCACTCTCCCGTGAACTTTACCCGGTGGTGCTATCGGG 15872 962 GTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGAAAAGAGC 1015 15871 GATGAAAGCTGGCGATGATGACCACCGATATGGCCGGTCTCCGTTATCGGG 15812	1016 GTTCATTTCAATAAACCGGGCGACCTCAGCCATCCTGGATTTTCCGCTTTCCAGCG 1075 15811 GAAGAAGTGGCTGATCTCAGCCACCGCGAAATGACATCAAAACGCCATTAACCTGATG 15752 1076 TTCGGCACGAGACGACGACGACCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGAT 1132 15751 TTCTGGGGAATATAAATGTCAGGCTCCCTTATACCAGCCAGTCTGCAGGT 15701 1133 ATTGACATCATAATACCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTAAATA 1192	cgaracagragaaattacagaaaactttatcacgtttagtaagtatagaggtgaaaatcc cgaracagaacacctctttttgacatacttcgggtagtgccgatcaacgcc cgatcaaagccaaagcacacctctgtaaaagtataagagtatcaagagacaccaagagttatat cattttcgccaaaagttggcccaaggcttccggtatcaacagagacaccaagattatat catttttcgccaaaagttggcccaaggcttcccggtatcaacagagacaccaagattatat cattttcgccaaaagttggcccaaggcttcccggtatcaacagagacaccaagattatat cattttcgccaaaagttggcccaaggcttcccggtatcaacagagacaccaagattatatata
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	3737 AGACGATTCCGTTTGAGAAGAACATTTGGAAGCTGTCGGTCG	OY 3917 CAAAATCTAATTTAATATTGATATTTATATCGTTTTCGTTCTGGCTTTTTT 3976 Db 13097 CAAAATCTAATTTAATATTGATATTTATATCATTTTACGTTTCTGGTTCTAGCTTTTTT 13038 OY 3977 GTACAAAGTTGGC 3989 Db 13037 GTACAAACTTGTC 13025 RESULT 15	US-10-055-001A-24/C Sequence 24, Application US/10055001A Sequence 24, Application US/10055001A Publication No. US20030049835A1 GENERAL INFORMATION: APPLICANT: Weathouse, Peter APPLICANT: Helliwell, Christopher A. TITLE OF INVENTION: Wethod and means for producing efficient silencing constructs TITLE OF INVENTION: using recombinational cloning FILE REPERENCE: HELLGA CURRENT APPLICATION NUMBER: US/10/055,001A CURRENT PILING DATE: 2002-06-11 NUMBER OF SEO ID NOS: 26	SOFTWARE: Patentin version 3.1 SEQ ID NO 24 LENGTH: 17476 TYPE: DNA ORGANISM: Artificial sequence FEATURE: OTHER INFORMATION: acceptor vector phblilsGATE8	Query Match 22.4%; Score 1089.4; DB 15; Length 17476; Best Local Similarity 59.4%; Pred. No. 7.6e-157; Indels 243; Gaps 18; Matches 2314; Conservative 0; Mismatches 1336; Indels 243; Gaps 18; Oy 122 GCCAACTTGTACAAAAAAGGTGAAGGAGAAACGTAAAATGATATATAT

13797 CGACGGATGCTGATCCCCTGGCCAGTGCACTC 3289 CGATAACGCTCTTTTATAGGTGTAAACCT 13737 CTTTACCGGTGCATATCGGGATGAAAGCC 3343 CCTGTTCTGTCAGGAAAGGCCGTTCATTTG 13677 AGTGTGCGTCTCTCGTTATCGGGAAGAAGTGC 3403 TTCCTGATTTCCGCTTTATCGGGAAGAAGTGC 3403 TTCCTGATTTTCGCTTTATCGGGAAGAAGTGC 3403 TTCCTGATTTTCGGCTTTCCAGGGAAGAAGTGC 3460 GGTTGTGCTTACCAGAGATGTTCTGGGGAA	8 8 8 8 8 8 8	2149 TAACAAGCTAAAGTAACAAATAATCAAACTAATGAAACGTAATCTAATGTAACGAA 2208 14762 AAACCAGCTAAGAATTATTAACTAATGATTAATGATTATTATTTT 208 2209 ACATAATCTAATAACAAAGGGCAAGATCTATTATATATAT	
13971 AAGGGGAAAATCAGGAAGGGATGGCTGAGGTGG 3109 ACGGAGACCGGCACACTGGCCATATCGGTGGTG 13911 TTGCTGACGAGAACAGGGACTGGTGAAA 3169 TGCACCACGGTAAAGTTCACGGGAGACTTTAT 13857 AGAGGGCGTTATCGTCTTTTGTGGATGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	8 6 8 6 8	14942 IGAIAAATTACAAGCAGATTGGAATTCTAACAAATATTTATTAACTTTAAAGTAAA 14883 2029 AATAGTTATTATTAATTAAATTACTAACCATTACTAACATTTTAGTTTAAAAGTTA 2088 14882 TATTAGTAATGGTATAGATATTAATTATATATATATAATA	66666
2929 CTGGATTTTCAGCCTCTATACTTACTAACGTGG 14088 GTGACAGTTGACAGCACACAGCTATCAGTTGCTGC 2989 CGACCTGCAGACTGGCTGTGTATAAGGAGCCTC 14028 GTCTGGTAAGCACACCATGCAGAATGAAGCCCC	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	1849 GTTGAGAGTAAGTATATTTTTAATGAATTTGATGAAGATGTAAGATGAT	8 6 8 6
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CAAGGCATATATGATGTCAATATCTCCG 14029 AGCTGGATGGCAAATAATGATTTTATTT 2508 ------TCCTCGAGACC 14446 GGCCAACTTTGGCGAAAATGAGACGTT 14146 carcarcacarace---gaacecrada 13972 AATGCAĞTTTAAĞGTTTACACCTATAAA 13858 ACAGAGTGATATTATTGACACGCCGGG 13798 GGCTGATCTCAGCCACGGGAAAATGAC 13618 aararaaargrcaggcrcccrraracac 13558 AAATGATATAAATATCAATATATTAAAT 14386 CTGTAAACACAATATCCAGTCACTA 14326 GTAGTCGACTAAGTTGGCAGCATCACCC 14266 Gregerareak---ecacceratraca 14089 decederitarteaareaaeeeerer 13912 rcigcrgrcagaraaagrcrccgrgaa 13738 cregececareargaceacearargece 13678 AAATGATATAAATATCAATATATAAAT 2628 CTGTAAAACACATATCCAGTCACTA 2688 GTAGTCGACTAAGTTGGCAGCATCACCC 2748 GGAAGATCACTTCGCAGAATAAATAAAT 2808 GGCCAACTTTTGGCGAAAATGAGACGTT 2868 TTTTCTCTTACAAGTCGTTCGGCTTCAT 2928 GATAAAGTTTCTGTAATTTCTACTGTAT 2988 TGACATTTATATTCCCCAGAACATCAGG 3048 GCTGAGATCAGCCACTTCTTCCCCGATA 3108 CATCATGCGCCAGCTTTCATCCCCGATA 3168 ATCTGACAGCAGACGTGCACTGGCCAGG 3228 AATATCACTCTGTACATCCACAAACAGA 3288 CTTAAACTGCATTTCACC-----AGTC 3342 IGATAAGCAATGCTTTCTTATAATGCCA 2568 CAATAAACCGGGCGACCTCAGCCATCCC 3402 CATCATATATGCCTTGAGCAACTGATAG 3516 CACGCAGACGACGGCTTCATTCTGCAT 3459 TIGATIACAGIIGGGAAGCIGGGIICGA 2448

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13137 TATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATT 13078
13437 AATTGTTCTTGATGCAGATGATTTTCAGGACTATGACACTAGCGTATATGAATAGGTAGA 13378
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                                                                                                                                                                                                                                                                                                                                            3817 GGCTGTCGGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGA 3876
                                          3517 CTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATAC 3576
                                                                                                      3577 TTCTGTTCTTGATGCAGATGATTTTCAGGACTATGACACTAGGGTATATGAATAGGTAGA 3636
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: May 8, 2004, 10:19:35 ; Search time 7543.25 Seconds (without alignments) 19251.609 Million cell updates/sec	score: US-10-055-001B-23_COPY_1300 =: 1 ttcatttggagagacacg table: IDENTITY_NUC Gapop_10.0, Gapext_1.0 1: 27513289 segs, 14931090276 umber of hits satisfying chosen para DB seg_length: 0	seq lengt Max Max Lis Lis 2: 2: 2: 6: 6: 6: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:	13: gb_est4:* 15: em_estfin.* 15: em_estfin.* 16: em_estfin.* 17: em_gss_lnm:* 18: em_gss_vrt:* 20: em_gss_vrt:* 21: em_gss_rns:* 22: em_gss_rns:* 23: em_gss_pro:* 24: em_gss_pro:* 25: em_gss_pro:* 26: em_gss_pro:* 27: em_gss_pro:* 28: gb_gss_r:* 29: gb_gss_r:* 20: gb_gss_r:*	Result Query Out Score March Length DB ID Description 1 518.4 10.7 698 29 AG012840 AG012840 Homo sapi 2 496.6 10.2 713 29 AG000762 AG000762 Homo sapi 3 437.2 9.0 542 14 CD109790 CD109790 AG000761 Homo sapi C 4 411.8 8.5 723 29 AG000761 AG000761 Homo sapi

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                          679 TATTCCCCAGAACATCAGGTTAATGGCGTTTTTTGATGTCATTTTCGCGGTGGCTGAGATC
                                                                                                                                                                                                                                                                                                                               599 TATATCCCCGGANCATCNGTTAATGCCGTTTTTGAAGGNATTTTCGCCGTGGCTGAGAAT
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                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                29;
                                                                                                                                                                                                              Score 496.6; DB 29;
Pred. No. 7.9e-78;
0; Mismatches 30;
Tel:0427-78-9732, Fax:0427-78-9561)
                                  1. 713

Organism="Homo sapiens"

(organism="Homo sapiens"

/or_type="genomic DNA"

/db_xref="reaxon:9606"

/chromosome="21"
                    Location/Qualifiers
                                                                                                                                                       /clone="64E11X4"
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llarity 94.2%;
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Homo sapiens
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Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (B-mail:hattori@hgc.ims.u-tokyo.ac.jp,
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Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published only in DataBase (1997)
2 (bases 1 to 713)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                           94 GATCAGCCACTICTICCCCGATAACGGAGACCGGCACACTGGCCATAICGGTGGTCATCA
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                                                                                                                                                                                              TTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTTGATGTCATTTTCGCGGTGGCTGA
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Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
                                                                                                                                                         4
                                                                                                              Length 698;
                                                                                                              Score 518.4; DB 29; Length
Pred. No. 1.1e-81;
0; Mismatches 2; Indels
db xref="taxon:9606"
                                      /map="21q"
/clone="f65H12X16"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 723)

L Published Only in DataBase (1997)

E 2 (bases 1 to 723)

S Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

L Published Only in DataBase (1997)

E 2 (bases 1 to 723)

S Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

Direct Submission

Submitted (31-0CT-1997) Masahira Hattori, Kitasato University, Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:042-78-9561)
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                                                          AG000761 723 bp DNA linear GSS 06-FE.
Homo sapiens genomic DNA, 21g region, clone: 64B11X4, genomic
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98.1%; Pred. No. 7.7e-63;
live 0; Mismatches 8;
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                                                                                                                                                                                         AG000761.1 GI:2579569
                                                                                                                                                                                                                                                       Homo sapiens (human)
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Matches 416; Conservative
                                                                                                                           survey sequence. AG000761
                                                                                                                                                                                                                                                                                          Homo sapiens
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/tissue_type="Human Placenta"
/tish host="NHIOB TonA"
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/note="Organ: placenta; Vector: pBluescriptR; Site_1:
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1062 TCCGCTTTCCA-GCGTTCGGCACGCAGGACG-ACGGGCTTCATTC--TGCATGGTTGTGCT 1117
                    Tissue Procurement: Dr. Stefan Hansson characteristics of the procurement: Dr. Stefan Hansson characteristics of the preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.4G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation (Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 24 High quality sequence start: 144 High quality sequence start: 144 High quality sequence stop: 251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
smail: cgapbs-r@mail.nih.gov
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Best Local Similarity 95.5%;
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninoi (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: NDAM991 row: e column: 05
High quality sequence start: 68
High quality sequence stop: 256.
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/clone lib="NIH MGC 148"
/clone lib="NIH MGC 148"
/clone lib="NIH MGC 148"
/clone lib="NITH TOTATT 3. size lesselected for average insert alr-Xhoi; Site 2: BamH; Library is oligo-dT primed and directionally cloned using primer
5. TTTTTTTTTTTTTTTTTTTTTTTY 3, size-selected for average insert size 2:3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap trapper method (Carninoi, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC
                                                                                                                                                   EST 01-MAY-2003
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                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 TGGCGTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCCGATAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCCCGATATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                             CB997937 522 bp mRNA linear ES:
AGENCOURT_13894516 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 404; DB 14; Length 522;
Pred. No. 2.1e-61;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .522
/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
189 TTTTGACATACTTCGGGTA 170
                                                                                                                                                                                                                                                     CB997937.1 GI:30292457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1154 AGCAACTGATAGCTGTCGCTGTCAACTGTAATACGCTGCTTCATAGCACACCTC 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           974 AACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCG 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTG 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-SEP-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Teas:0427-78-9561)
On Peb 5, 1999 this sequence version replaced gi:2951836.
AG005773: Submitted (11-Mar-1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 ACAGCAGACGTGCACTGGCCAAGGGGGATCACCATCCGTNGCCCGGGCGTGTC-ATANTA 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             426 AACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
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                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (hases 1 to 725)

Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNA, chromosome 21q

Published Only in DataBase (1998)

2. (bases 1 to 725)

Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                676 TTATATTTCCCCAGAACATCAGGTTAATGGCGTTTTTTGATGTCATTTTCGCGGTGGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               723 TYNATATCCCCGGANCATCAGNTTAANGCGTTTTTTGGAAGCCATTTTCGCGGTGGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 GGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC--ATATGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         663 ATCAGCNANTITICCCCGRATAANGNAGACGCCACANTGCCNATATCNGNIGITCATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603 GCGCCAGCTTTCATCCCCCAATA-GCACCACGGGGTAANGTTCACGGGAGAACTTTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGCAGACGTGCACTGGCC-AGGGGGATCACCATCGGTCGCCGGGGGGTGTCAATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              914 TCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTTTATAGGTGTAAACCTTA
     Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="21q"
/clone="f32E9X13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="21"
                                                                          AG013450.1 GI:3549208
GSS.
                                                                                                                                 sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505; Conservative
                                 survey sequence.
AG013450 AG005773
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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Lil, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Endress, G.M., Lil, S., Jacotot, E., Bartin, N., Janky, R., Moore, T., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M. Huang, R., Chance, M. R., Lee, H., C. elegans Orreme version 1.1: experimental verification of the genome annotation and resource for protecome-scale protein
                                          1056
                                                                                                                                                                                                                       1117 TTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTC 1176
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;
                                                                                                                                GATITICCGCTTTCCAGCGTTCGGCACGCACGCACGACGGCTTCATTCTGCATGGTTGTGC 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB395230 487 bp mRNA linear EST 15-MAY-2003 OSTR151B2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
                                                                                    371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
pOLYÃ=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev stage="mixed stage" /clone_lib="AD-wrmcDNA" /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The CDNAs were cloned into pPC86"
                                                                                                                                                          370 GATTTTCCGCTTTCCAGCGTTCGGCACACGACGACGGCTTCATTCTGCATGGTTGTGC 311
                                                                                                                                                                                                                                                                   254
489 ACGATAACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGT 430
                                                                                                                                                                                                                                                                                                             1177 AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATACTTCGGGTA 1233
                                                                                                                                                                                                                                                                                                                                            253 AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTA 197
                                                                                                                                                                                                                                                310 TTACCAGACCGGAGATATTGACATC--ATATGCCTTGAGCAACTGATAG-TGTCGCTGTC
                                          TCTCGTCAGCAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCT
                                                                                 429 reregreage-aagageegrreatricaraaaceggeegeereageeareerreer
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H
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Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
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Pred. No. 4.3e-53;
0; Mismatches 25;
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/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Contact: Vidal M
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Best Local Similarity 93.6%;
Matches 383; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (31-007-1997) Masahira Hattori, Kitasato University, Department of Science, JGT Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail.hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
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                                                     263 TCACCATCCGTCGCCCGGGCGTGTCAATATCACTCTGTACATCCACAAACAGACGAT 322
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I (bases I to 722)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1997)
Attori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Direct Submission
                                                                                                    942 AACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTAATGGCGTTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AG000763 722 bp DNA linear GSS 06-FEI
Homo sapiens genomic DNA, 21q region, clone: 64E11X4, genomic
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Pred. No. 1.8e-60;
); Mismatches 31; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="64E11X4"
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Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitti, J., Doucette-Zamm, L., Hartley, J.L., Temple, G.F., Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-2001
/clone_lib="AD-wrmcDNA" library was generated with poly(A)+ note="The AD-wrmcDNA library was generated with poly(A)+ NA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
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Dana Farber Cancer Institute
4 Binney Street, Boston, MA 02115, USA
Tel: 617 632 2425
Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
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                                                                                                                                                                                          Score 347.4; DB 14; Length 487;
Pred. No. 2.1e-51;
0; Mismatches 11; Indels 1;
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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F11F1.5, mRNA sequence.
B1174407
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96.88;
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Matches 365; Conservative
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
POLYA-NO.
                         215
                                                          TAAAATGATATAAATATATATATAAATAAGATTTTGCATAAAAAACAGACTACATAA 428
                                                                                                                      275
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Caenorhabditis elegans
Enkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditodea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 487)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORPeome version 1.1: experimental verification of the
genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                               CTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACC 335
                                                                                                                                                                                                                                                                                                         GACAGCCTTCCAAATGTTCTTCTAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGT 395
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                                                                                                                                                                                                                                                    CTGTAGTCGACGGACAGCCTTCCAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACC
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                                                                                                               TACTGTAAAACACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGAC
                    TAAAATGATATAAATATCAATATTAATTAAATTTAGATTTTGCATAAAAAACAGACTACATAA
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Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
Tel: 617 632 5180

    .487
    organism="Caenorhabditis elegans"

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CB395230
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FEATURES

TITLE

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us-10-055-001b-23 copy 13000 17862.rst

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3580 IGTICTIGAIGCAGAIGAITITCAGGACIAIGACACIAGCGIAIAIGAIAGGIAGAIGI 3639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3820 TGTCGGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGATAT 3879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. ESTS of Japanese morning glory
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                /close_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were closed into pPC86"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eŭkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids, Solanales; Convolvulaceae; Ipomoea.

[ Dases 1 to 337]
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44 Binney Street, Boston, MA UZILL, CL. Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 384;
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                                                                                                                                                                                                                                       /organism="Caenorhabditis elegans"
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/strain="N2"
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Pred. No. 1.8e-47;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                      /sex="Hermaphrodite and male"
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                                                                                                                                                      philippe vaglio@dfci.harvard.edu-
POLYA=No.
                                                                                                                                                                                                                                                                                                     /db xref="taxon:6239"
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Best Local Similarity 98.2%;
Matches 329; Conservative
                                                                                                                                                                                                                      1. .384
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Best Local Similarity
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                                                                                                                                               /db_xref="taxon:6239"
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RNA isolated from both hermaphrodite and male N2 worms of
subsequent generation of cDhAs by poly(A) priming. The
cDNAs were closed into ppC86"
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                                                                                          organism="Caenorhabditis elegans"
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        philippe_vaglio@dfci.harvard.edu
POLYA=No.
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Marc Vidal Laboratory
Dana Farber Cancer Institute
                                                 Location/Qualifiers
                                                                                                         /mol_type="mRNA"
/strain="N2"
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LTADALLY 1037 bp mRNA linear EST 05-SEP-2003 P16A8 Plasmodium yoelli 17X axenic hepatic stages Plasmodium yoelii yoelii cDNA, mRNA sequence.
                                                                                                                                                                                             /clone lib="Plasmodium yoelli 17X axenic hepatic stages" /clone lib="Plasmodium yoelli 17X sporozoites were isolated from salivary glands of 17X sporozoites were isolated from salivary glands of infected Anospheles stephensi mosquitoes and purified over a DES2 cellulose column. The sporozoites were cultured for 24h at 37C in the presence of 5% CO2 and 10% FBS as described in Transformation of sporozoites into early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               726
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                                                                                                                                                                                                                                                                                                                                                       excertthroctic malazian parasites does not require host cells '(J Exp Med. (2003)197(8):1045-50). mRNA was extracted using the Invitrogen microFAST TRACK kit and used for cDNA construction via the BDBiosciences SWART CDNA synthesis kit. Double stranded cDNA was cloned into plasmid vector using Invitrogen's TOPO TA vector cloning
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Hasmodium yoelii yoelii
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1037)
Mangro, Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,
Nussenzweig, V. and Bhanot, P.
Expressed sequence tags from Plasmodium yoelii hepatic stages in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 AANAATATCGCTCGGNNCATCCACNANCNNANGANANCGGCTNTNTTTCACAGGTGNA
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                                           'organism="Plasmodium yoelii"
                                                                                                         /sub_species="yoelli"
/db_xref="taxon:73239"
/ds_trage="axenic hepatic stages"
/lab_host="E. coli TOP10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.6%; Score 273.2; DB 14
90.0%; Pred. No. 2.2e-38;
iive 0; Mismatches 31;
Location/Qualifiers
                                                                     type="mRNA"
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Department of Pathology
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                                                                                                                                                                                                                                                                                                /clone="jm18n08"
/tissue_type="mixture of flower and flower bud"
/clone_lib="Tpomoea nil mixture of flower and flower bud"
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similar to NR|GI-23483806 hypothetical protein [Flasmodium yoelii
yoelii] (e-108).
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Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1068)
Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,
Nussenzweig, V. and Bhanot, P.
Expressed sequence tags from Plasmodium yoelii hepatic stages in
axenic culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     702 TGGCGTTTTTTGATGTCATTTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGG
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Department of Pathology
New York University School of Medicine
550 Users Avenue, MSB 131, New York, NY 10016,
Fal: 212 263 5346
Fax: 212 263 8179
                   Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                    /organism="Ipomoea nil"
|nol_type="mmky"
|cultivar="Tokyo-kokei standard"
|db_xref="taxon:35883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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/de_stage="axenic hepatic stages"
//de_stage="axenic hepatic stages"
/lab_host="E. coli TOP10"
/clone_lib="Plasmodium yoelli 17X axenic hepatic stages"
/clone_lib="plasmodium yoelli 17X axenic hepatic stages"
/note="Vector: pCR4,0TOP0; 10 million plasmodium yoelli
17X sporozoites were isolated from salivary glands of
infected Anospheles stephensi mosquitoes and purified over
a DE52 cellulose column. The sporozoites were cultured for
24h at 37C in the presence of 5% CO2 and 10% FBS as
described in Transformation of sporozoites into early
exocrythrocytic malaria parasites does not require host
cells (T Exp Med (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microPAST TRACK kit and
used for cDNA construction via the BDBiosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 06-FEB-1999
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New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanopolemed.nyu.edu
No Blast Hits ().
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/organism="Plasmodium yoelii yoelii"
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/strain="17X"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 724)

AG000791.1 GI:2579599 Homo sapiens (human) Homo sapiens

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

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             Published Only in DataBase (1997)
2 (Dases 1 to 724)
2 (Dases 1 to 724)
3 (Dases 1 to 724)
4 Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:Battori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
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98.6%; Pred. No. 8.9e-37;
iive 0; Mismatches 1
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	CVE311874 BD263377 BD263381 BD263402 BD263380 BD263379 BD263378	CVB311872 CVB311873 BD263382 BD194641 FTPDKG AZ3998 AZ4783 AR074388 AZ4782 AR074388 AZ4782 AR074387 AR074387 AX310901 CVB18556	AX063413 AX063413 AX063413 AR098312 AR098312 149885 182373 AX012337 AX007512 AX007512 AX052541 AX310333	ATACAS BO0404 BO0546 BO0546 BASS 4803 BD016312 AF242881 AF433042 AF433042 AF433042 AF184978 AY2184978 AY2184978 AY2184787 ATU414109 ATU414109 ALIGNMENTS	18691 bp DNA 15982218 stance protein; neomycin speC gene; spectinomyci pHELLSGATE pHELLSGATE annces; vectors.
Y Sh Length DB	18691 18691 8 44470 8 5584 1 4165 2 4208	4 4 4 4 4 7 4 8 8 8 8 8 8 8 8	8.000000000000000000000000000000000000	24595 8 24595 8 24595 8 24595 6 6 8 24595 6 6 8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	or GI: sisis sisis hi7. or cor equ
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13121 GCCAACTTTGTACAAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATTT 13180
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GRLGVADRYQDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 ACTAIGAATCAACTACTTAGAIGGTATTAGIGACCTGIAGTCGACCGACCGACAGCCTICCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTATACTTTTCCTTACAAGTCGTTCGGCTTCATCTGGGTTTTTCAGCCTCTATACTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATCAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACACAACATTCCAGTC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 AGAAATAAGAAAAAGAGGGGAGCCTCTTTTTGTGTGTGACAAAATAAAAACATCTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC
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/note="octopine esynthase (ocs) terminator"
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llarity 79.5%; Pred. No. 0;
Conservative 0; Mismatches
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/function="35S promoter"
14660. .16258
                                                                            1443. .2148
/note="NOS terminator"
2149. .2706
/note="left border"
7793. .9388
                                                                                                                                                                                                                                                            /transposon="Tn7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1/transl_table=11
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/gene="spec"
8600. .9388
/gene="spec"
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/
Gleave, A.P., Green, A.G. and Waterhouse, P.M.
Construct design for efficient, effective and high-throughput gene silencing in plants
Plant J. 27 (6), 581-590 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="pHELLSGATE is a derivative of cloning vector
pART27"
                                                                                                                                                                11576441.
2 (bases 1 to 18691)
2 (bases 1 to 18691)
Waterhouse, P. M.
Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
..~ "Actor PHELLSGATE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="neomycin phosphotransferase II (nptII)"
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/organism="Agrobacterium tumefaciens"

/mol_type="other DNA"

/db_xref="taxon:358"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Cloning vector pHELLSGATE"
/mol_type="other DNA"
/db xref="taxon:167049"
/lab_host="Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Agrobacterium tumefaciens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Escherichia coli K12"
/mol_type="other DNA"
/strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Cauliflower mosaic
/mol_type="other DNA"
/db_xref="taxon:10641"
14660..16258
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/organism="Flaveria trinervia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Escherichia coli"
/mol_type="other DNA"
/db_xref="taxon:562"
9389. .11673
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/mol_type="other DNA"
/db_xref="taxon:562"
1443...7792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:83333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="other DNA"
/db_xref="taxon:4227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="other DNA"
/db_xref="taxon:358"
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trans table=
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PF 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR 28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO I
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       TIGIGCACGITGIAAAAACCIGAGCAIGIGIAGCICAGAICCITACCGCCGGITICGGI
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JP 2002537790-A/155.
synthetic construct
artificial sequences.
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Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning on
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by JC 2002537790-A/159
PD 12-NOV-2000
PD 12-NOV-2000
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/126049 PR 28-MAY-1999 US 60/136744
PL JAMES L HARTLEY MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC CI2N15/09,CO7K14/00,CI2N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/PC
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Compositions and methods for use in recombinational cloning of nucleic acids.
N BD263381
BD263381.1 GI:33073149
SPACE COMPOSITION CONSTRUCT
SM SYNTHETIC CONSTRUCT
SM SYNTHETIC CONSTRUCT
Artificial sequences.
E 1 Chaps. 1. L. Brasch, M.A., Temple, G.F. and Cheo, D. Compositions and methods for use in recombinational cloning of
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Location/Qualifiers
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/organism="synthetic construct"
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Patent: JP 2002537790-A 159 12-NOV-2002;
INVITROGEN CORP
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JP 2002537790-A/158.
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Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning of
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Patent: JP 2002537790-A 158 12-NOV-2002;
INVITROGEN CORP
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PN JP 2002537790-A/158
PP 02-MAR-2000 JP 2000602252
PP 02-MAR-1999 US 60/122389,23-MAR-1999 US 28-MAY-1999 US 60/136744
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Synthetic construct

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Compositions and methods for use in recombinational cloning of compositions and methods for use in recombinational cloning of nucleic acids

RS Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.

Compositions and methods for use in recombinational cloning of nucleic acids

RS Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.

RS Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.

AL 10 2002337790-A 180 12-NOV-2002;

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PR 12-NOV-2002

PR 02-MAR-1999 US 60/122389, 23-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/136744

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PR 02-MAR-1999 US 60/136744

PR 02-MAR-1999 US 60/136744

PR 02-MAR-1999 US 60/136744

PR 02-MAR-1999 US 60/136744

PR 02-MAR-1999 US 60/12288/10, CI2NI/19, CI2NI/19, CI2NI/21, CI2NIS/10, CI2NIS/ PC 00, CI2NIS/00

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA
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1. .5584
/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1108.8; DB 6
Pred. No. 6.9e-151;
0; Mismatches 2;
                                 4747
                   4716 ATAGCACACCTCTTTTTGACATACTTCGGGTA
1106 ATAGCACACCTCTTTTGACATACTTCGGGTA
                                                                                                                              bp
use
                                                                                                                              BD263402
Compositions and methods for nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.8%;
Best Local Similarity 99.8%;
Matches 1110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
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                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                          RESULT 4
BD263402/c
                                                                                                                                               DEFINITION
                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                      TITLE
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wethods for use in recombinational cloning completed. F. and Cheo.D. methods for use in recombinational cloning comparisons.

**ITROGRAM CORP.**

OS Artificial Sequence DN UP 2002537790-A/157

PD 12-NOV-2002

PF 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/128744

PF 02-MAR-1999 US 60/136744

PF 02-MAR-1999 US 60/138745, CL2N1/19, CL2N1/21, CL2NS/10, CL2NIS/ PC CLANS/09, CONTAL/19, CL2NI/19, CL2NI/12, CL2NIS/ PC CLANS/09/CNX/44/00, CL2NI/15, CL2NI/19, CL2NI/21, CL2NIS/ PC CLANS/09/CNX/44/00, CL2NI/15, CL2NI/19, CL2NI/21, CL2NIS/ PC CLANS/09/CNX/44/00, CL2NI/15, CL2NI/19, CL2NI/21, CL2NIS/ PC CC ALTP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4208 bp DNA linear PAT 17-JUL-2003 and methods for use in recombinational cloning of
                                      CATTCTGCATGGTTGTGCTT 3180
                                                                                 3024 TITICCGCTTTCCAGCGTTCGGCACGCAGCACGACGACTTCTTCTGCATGCTTGTGCTT 3083
                                                                                                                                                                                                                         3084 ACCAGACGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAA 3143
                                                                                                                                                                                                                                                                                                                                  CTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCTTGAT 3300
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                                                                                                                                                                                                                                                                                                                                                                             3144 CIGICACIGIPATACGCIGCITCAIAGCACACCTCTITIIGACATACITGGGGTATACAT
                                                                                                                                                                                      ACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGTGTCAA
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/organism="synthetic construct"
/mol_type="genomic DNA"
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Location/Qualifiers
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BD263379.1 GI:33073147
JP 2002537790-A/157.
Synthetic construct
synthetic construct
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Matches
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BD263379
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PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC C12NN15/09, C07KN14/00, C12NN1/19, C12NN1/21, C12NN5/10, C12NN15/ PC 00, C12NN5/09, C07 CC PDONR204

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/organism="synthetic construct"
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1 (bases 1 to 4204)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning of
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                                             Compositions and methods for use in recombinational cloning nucleic acids.
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IELDJANSGKILESFRPERFPRMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVB
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFKELTAFTHNGDHVTRL
DRWEPELNATIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
IRSAALPAGNFTADKSGAGERGSRGIIAALGPDGKPSRIVVITTGSQATMDERNRQIA
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|transl_table=11
|produce="ampillin resistance protein"
|protein_id="CAC86250.1"
|db_xref="G1:1598215"
|db_xref="G1:1598215"
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Plant J. 27 (6), 581-590 (2001)
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                                                                                                                          AAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTTCCGC
                                                                                                                                                                              TTTCCAGCGTTCGGCACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACC
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AMP gene; ampicillin resistance protein; pdk gene; promoter. Cloning vector pHANNIBAL
Cloning vector pHANNIBAL
artificial sequences; vectors.
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AUSTRALIA
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2601,
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/mol_type="other DNA"
/db_xref="taxon:358"
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/organism="cloning vector pHANNIBAL"
/mol_type="other DNA"
/db_xref="taxon:167047"
/lab_host="Escherichia coli"
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Submitted (04-MAY-2001) Waterhouse P.M.,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Escherichia coli K12'
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/organism="Flaveria trinervia"
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/db_xref="taxon:10641"
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/db_xref="taxon:4227"
5049. .5814
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/strain="Kl2"
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AJ311872
AJ311872.1 GI:15982214
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2 (bases 1 to 5824)
Waterhouse, P.M.
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/trānslation="MAKMRISPELKKLIEKYRCVKDTEGMSPAKYYKLVGENENLYLK
NIDSRXKGTTYDVEREXDMIWLEGYLIPVPKYLHFERHDGMSNLLMSBADGVLCSBEY
EDDGSPEKTIELYABCTRLHFRIDISDCPYNNSLDSRLABLDYLLNNDLADVDCENWE
EDTPFVDPRELYDFKTEKPERELVPSHGDIGDCNIFYNDGKNGGFIDUGRSGRADKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4844 GITIAITATATAATTAATATCTATACCATTACTAAATATTTTAGTTTAAAAGTTAATAA 4903
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Pred. No. 8.6e-110;
0; Mismatches 66; Indels
                                                                                                                                          protein"
                                                                                                codon start=1
transT table=11
product="kanamycin resistance
                                                                                                                                                    protein id="CAC86251.1"

db xref="G1:15982217"

db xref="REMTREMBL:CAC86251"
                                                                                                                                                                                                                                                                                                          104. ,4449
function="358 promoter"
             ca
/gene="kan"
1075.
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4493. .5234
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/gene="kan"
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sinstruct design for efficient, effective and high-throughput gene silencing in plants
Plant J. 27 (6), 581-590 (2001)
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CTATTAATTAAATGAATTAGTCGAACATGAATAAACAAGGTAACATGATAGATCATGTCA
                                                                                                                                                                       CTATTAATTAAATGAATTAGTCGAACATGAATAAACAAGGTAACATGATAGATCATGTCA
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                                                         CAACATTCTTATTAATTCTAAATACTTGTAGTTTTATTAACTTCTAAATGGATTGA
                                                                                            CAACATICTTATTATTTCTAATTATACTTGTAGTTTTATTAACTTCTAAATGGATTGA
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Cloning vector pKANNIBAL
Cloning vector pKANNIBAL
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Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
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which was a derivative of pGEM-9ZE(-):
1. .3103
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/organism="Agrobacterium tumefaciens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mosaic virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Cloning vector pKANNIBAL"
/mol type="other DNA"
/db zeref="taxon:167048"
/lab_host="Bscherichia coli"
                                                                                                                                                                                                                                                                                                                                                               ATATAAATATATATATATAAATTAGATTTTGCATAAAAAC
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|mol_type="other DNA"
|db_xref="taxon:4227"
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'organism="Cauliflower
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3104. .4449
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'db_xref="taxon:10641"
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'strain="K12"
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Cloning vector pKANNIBAL.
AJ311873
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	4. 4. 4.		Db 4436 GGAGATATTGACATCATATGAGCAACTGATAGCTGCGCTGCACTCACT	REPERENCE 1 (Dages 1 to 786) AUTHORS Materhouse, P.M., Wang, M.B. and Graham, M.W. TITLE Method and means of obtaining improved phenotype JOURNAL Patent: JP 2002511258 A 7 16-APR-2002; COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION OS Artificial Sequence No JP 2002511258-A/7 PD 16-APR-2002 PP 07-APR-1999 JP 2000543598 PR 08-APR-1999 US 09/056767,03-AUG-1998 US 09/127735 PI PPTER MICHAEL WATERHOUSE, MIN BO WANG, MICHAEL WAIN GRAHAM PC CIZNIS/09, A01H5/00, CIZNIS/10, CIZNIS/00, CIZNIS/00 CC Description of
5024 2085 5084 2145 5144 5205	OY 2265 GATAAGCTTGGATCCTCTAGACCACTTTGTACAAGAAAGCTGAACGAGAAAAGG 2324 Db 5264 GATAAGCTTGGATCCTCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCTATGATCGC 5323 OY 2325 ATATAAATATCAATATTAAATTAGAATATGCATAAAAAAC 2366 Db 5324 ATGATATTGCTTTCAATTCTGTTGCACGTTGTAAAAAAC 5365 RESULT 10 BD263382/c	LOCUS BD263382 BD263382 DEFINITION Compositions and methods for use in recombinational cloning of nucleic acide. ACCESSION BD263382 BD263382 BD263382 BD263382 BD263382 BD263382 SOURCE ORGANISM SYNTHetic construct ATTICE COMPOSITIONS AUTHORS JOURNAL INVITROGEN COMPOSITIONS AUTHORS AUTHORS COMMENT SALTIFICIAL SALTIFICATION SALTIFICIAL COMMENT SALTIFICATION SALTIFICATION SALTIFICATION SALTIFICATION SALTIFICATION SALTIFICATION SALTIFICATION SALTIFICATION SET SEQUENCE BD 12-NOV-2002	ourc	ORIGIN Query Match 18.4%; Score 823.8; DB 6; Length 5156; Best Local Similarity 99.8%; Pred. No. 1.1e-109; Matches 825; Conservative 0; Mismatches 2; Indels 0; Gaps 0; QY 311 TATTAAATCATAAAAGAAATAAGAAAAAAGAGGGGCCCCTTTTTTGTGTGACAAAA 370 Db 5156 TATTAAATCATAAAAGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAAA 5097 QY 371 TAAAAACATCTACCTATTCATAAACAGTGTCATAGTCCTGAAAATCATCTGCATCAA 430

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Artificial Sequence: intron 2 of the Flaveria trinervia CC puryvate orthophosphate dikinase Location/Qualifiers FT source //organism=/Artificial Seq FT
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ilarity 100.0%; Pred. No. 3.1e-103;
Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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PLN 15-APR-1996

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Flaveria trinervia
Flaveria trinervia
Rekaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                   Rosche, E., Strenbel, M. and Westhoff, P.
Fighnary structure of the photosynthetic pyruvate orthophosphate diktinase of the C3 plant Flaveria pringlei and expression analysis of pyruvate orthophosphate diktinase sequences in C3, C3-C4 and C4 plant mol. Biol. 26 (2), 763-769 (1994)
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9324. 9486,9737. 9972,10177. 10305,10401. 10580,
10735. 10872,10947. 11111,11221. 11382,11480. 11569,
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join(1212. 1346,1481. 1733,7839. 7895,9093. 9230,
9224. 9486,9737. 9972,10177. 10305,40401. 10580,
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Birect Submission
Submitted (03-MAY-1994) E. Rosche, Institut f. Entwicklungs-
Molekular-, biologie der Pflanzen, Heinrich-Heine-Universitaet,
Universitaetsstr. 1, 40225 Duesseldorf, FRG
Location/Qualifiers
  trinervia pdk gene for pyruvate, orthophosphate dikinase.
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RGGMTSHAAVVARGWGKCCVSGCADIRVNDNKIFTIGDPVIREDDMLSLTGEVI
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EYKVOTMI EI PRAALI AEEIGKEADFISFGTNDLITOMTFGYSRDDVGKFLQI YLAQGI
LOHDPFEVIDQKGVGQLIKMATEKGRAANPSLKVGI CGEHGGEPSSVAFFDGVGLDYV
SCSFFRVPIARLAAAQVIV"
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MFFASDERI KAVRKMIMAVTPEQRKVALDLLLPYQRSDFEGI FRAMDGLPVTIRLLDP
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VFGNMGNTSGTGVLFTRNPSTGEKKLYGEFLINAQGEDVVAGIRTPEDLGTMETCMPE
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Activation-tagging vector pSKI015
artificial sequences; vectors.

1 (bases 1 to 10138)
Weigel,D., Ahn,J.H., Blazquez,M.A., Borevitz,J.O.,
Christensen,S.K., Fankhauser,C., Ferrandiz,C., Kardailsky,I.,
Malancharuvil,E.J., Neff,M.M., Nguyen,J.T., Sato,S., Wang,Z.,
Xia,Y., Dixon,R.A., Harrison,M.J., Lamb,C.J., Yanofsky,M.F. and
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                                                             GCATGATATTTGCTTTCAATTCTGTTGTGCACGTTGTAAAAAAACCTGAGCATGTGTAGGCT
                                                                                                    CAGATCCTTACCGCCGGTTTCGGTTCCATTCTAATGAATATATCACCCGTTACTATCGTAT
                                                                                                                              CAGATCCTTACCGCCGGTTTCGGTTCTAATGAATATATCACCCGTTACTATCGTAT
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Plant Physiol. 122 (4), 1003-1013 (2000)
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Pred. No. 1.3e-98;
0; Mismatches 44
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Nazarov, V., Botterman, J., Stanssens, P. A novel ribonuclease and its inhibitor Patent: EP 0537399-A 3 21.APR-1993;
PLANT GENETIC SYSTEMS, N.V
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AUTHORS Kardailsky,I. and Weigel,D. TITLE Direct Submission JOURNAL Submitted (17-SEP-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La CA 92037, USA FEATURES Source 1. 10138 Mol type="genomic DNA" Mol type="genomic DNA" Mol type="genomic DNA" Mol type="genomic DNA" Mol type="genomic DNA" Mol type="genomic DNA" Mol type="derived from pUC19" misc_feature 2662 Misc_feature 2663. 2862 misc_feature 2663. 2829	misc_feature /note="derived from pUC19" misc_feature 28302849 misc_feature 28444178 misc_feature 28444178 misc_feature 42704294 misc_feature 42704294 misc_feature 76907113 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 7690713 misc_feature 76948784) misc_feature 7690713	ORIGIN ORECTLYTHILKSLEAGGEKSVVAVIGEPNDPSVRMFEALGYAPRAGEKREANHD OSTATTHILKSLEAGGEKSVVAVIGEPNDPSVRMFEALGYAPRAGEKREANHD OSTATTHILKSLEAGGEKSVVAVIGEPNDPSVRMFEALGYAPRAGEKREANHD OVERTY ORECT (431. 10119) Droduct="6" end and promoter" Droduct="6" end and promoter" Droduct="6" end and promoter" Droduct="6" end and promoter" Droduct="6" end and promoter" OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY Match OVERTY MAtch OVERY MAtch OVERTY MAtch OVERTY MAtch OVERTY MAtch OVERTY MAtch OVERTY MAtch OVERTY MA

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## ALIGNMENTS

Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds. Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24. (CSIR ) COMMONWEALTH SCI & IND RES ORG. Helliwell C; ABQ82141 standard; DNA; 17476 BP. 24-JAN-2002; 2002WO-AU000073. 26-JAN-2001; 2001US-0264067P. 29-NOV-2001; 2001US-0333743P. (first entry) Waterhouse P, WPI; 2002-682669/73. WO200259294-A1. 11-DEC-2002 01-AUG-2002. Synthetic. Wesley S, AB082141; ABQ82141 RESULT 

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA.

Claim 15; Page 74-83; 104pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria with a Bacherichia coli, (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites, (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

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fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention 

Sequence 17476 BP; 4490 A; 4369 C; 4343 G; 4274 T; 0 U; 0 Other;

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fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites.

The fracting with a same recombination site, and preferably are identical. The first and second recombination site, or the third and fourth recombination sites, do not recombination sites, or the third and same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors an also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide

sequence from the present invention

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13659 13059 13419 13719 13720 ATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGGACGTGCACTGGCCAG 13779 13359 13479 13539 13540 resacerseasacresersreraraassasseersaarrearrarareessassaasarea 13119 13179 13239 540 009 ñ 300 360 420 480 999 720 780 120 240 09 721 ATGCACCACCAGGTAAAGTTCACGGAGACTTTATCTGACAGCAGAGGCGTGCCACTGGCCAG AAAATGATATAAATATCAATATATATAAATTAGATTTTTGCATAAAAAAGAGACTACATAAT AACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCGGCTTTCATCCCGGAT 13000 TTTCATTTGGAGAGGACACGCTCGAGACAAGTTTGTACAAAAAAGCTGAACGAGAAACGT ACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC 13360 TGTGACAAAATAAAAACATCTACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCA 13420 rergearchaghacharricheachacherrhinereitrechtachagregerren 13480 renggarrincageereraracriaacraaacgrgaraaagritergraarrietaergra TCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCCAGAACATCAG 601 GITAATGGCGTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGAT 13600 GITAATGGCGTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGAT AACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCCAGCTTTCATCCCCGAT **AAAATGATATAAATATCAATATATATAAATTAGATTTTGCATAAAAACAGACTACATAAT** ACTIGIDADA CACADA CATATICCAGTICACTATIGA ATTICA CATACTAGATIGGTATTAGTICAC TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG reragiceacceacagecriceaaarericireegergarecreecaacriagiceacce ACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTC Acadecerrectatarierretetatacesateseresitatecaseeracreseratione crcaargccgrarraaarcaraaaagaaaraagaaaaagagagcgggccrcrrrrrg TGTGACAAAATAAAACATCTACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCA TCTGCATCAAGAACAATTTCACAACTCTTATACTTTTTCTCTTACAAGTCGTTCGGCCTTCA TCTGGATTTTCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTA 1 TITCATITIGGAGAGACACGCTCGAGACAAGTITGTACAAAAAAGCTGAACGAGAAACGT Gaps Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other; Length 17458; 18, 9; Indels DB 6; Score 4406.6; Pred. No. 0; 0; Mismatches 98.4**%**; 99.4**%**; Conservative Similarity Matches 4450; 541 661 121 301 61 13180 361 421 481 13060 13120 181 241 13240 13300 Query Match Local qq 임 d g à g δ a g Š 8 à à \$555555555555555555**X**& 엄 à a à qq ð 업 δ 엄  $\delta$ g à à

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bscherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-

Claim 16; Page 83-93; 104pp; English.

stranded RNA

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191   GGGGATUCACCATCCCTCGCCCGGGCCTGTAATATATATATATATAT	ATAATAGTAATTCTAGCTGGTTTCATGAATTAAATATCAATGATAAAATACTATAGTAAA 1800 ATAATAGTAATTCTAGCTGGTTTCATGAATTAAATATCAATGATAAAATACTATAGTAAA 1479 ATAAGAATAAATAAATAAATAAATAATTTTTTTTTTTATGATTAATATTAT

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region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and coll or by prokaryotic RNA polymerase; (ii) first, second, third and coll or by prokaryotic RNA polymerase; (iii) 3' transcription terminating and polyademylation region functional in the eukaryotic cell. The first and tecombination sites, or the second and third recombination sites and second recombination sites, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic and acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention

Sequence 17681 BP; 4586 A; 4402 C; 4374 G; 4319 T; 0 U; 0 Other;

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13719 13179 13359 13360 TGTGACAAATAAAAGATCTACTATTCATATACGCTAGTGTCATAGTCCTGAAAATCA 13419 13420 TCTGCATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCA 13479 13119 720 540 240 360 420 120 180 300 09 AACGGAGACCGGCACACTGGCCATATCGGTGGTCATGCGCCCAGCTTTCATCCCCGAT renggartrineageereraractraectraecereraagerrinergraatriceaceera TCGACCTGCAGACTGGCTGTGTATAAAGGGAGCCTGACATTTATATATTCCCCAGAACATCAG GTTAATGGCGTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGAT TCTGGATTTTCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTA TCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCCCCAGAACATCAG GITAATGGCGTTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGAT AACGGAGACCGGCACACTGGCCATATCGGTGGTCATGTGCGCCAGCTTTCATCCCCGAT ACAGCCTTCCAAATGTTCTTCTCAAACGGAATGGTCGTAATCCAAGCCTACTCGCTATTGTC AAAATGATATAAATATCAATATATTAAATTAGATTTTGCATAAAAAAAGAGACTACATAAT TGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG ACAGCCTTCCAAATGTTCTTCTAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTC CTCAATGCCGTATTAAATCATAAAAGAAATAAGAAAAAAGAGGTGCGAGCCTCTTTTTTG TGTGACAAAATAAAAACATCTACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATÇA TTTCATTTGGAGAGACACGCTCGAGACAGTTTGTACAAAAAGCTGAACGAGAAACGT ACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC TITCATITIGGAGAGACACGCICGAGACAAGIITGIACAAAAAAGCIGAACGAGAAACGI aaaatgatataaatatcaatattaaattagattttgcataaaaacagactacataat Gaps Indels 205; Length 17681; .. 0 DB 6; Score 4262; DB Pred. No. 0; 0; Mismatches 95.2%; Matches 4477; Conservative Similarity 601 661 13300 481 13480 541 13540 13600 H 301 361 421 13000 61 13060 181 13180 241 13240 Query Match Dp QQ QQ q  $\delta$ g qq ò Dp ò qq ₽ g  $\overset{\sim}{\circ}$ g  $\delta$ Dp Š Op ŏ õ

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14679 14740 ATAATAGTAATTCTAGCTGGTTTGATGAATTAAATATCAATGATAAAATACTATAGTAAA 14799 14379 14439 14559 14139 1500 14499 14619 1800 14319 1440 1560 1620 1680 1860 13959 14079 1200 1260 14259 096 14560 TATAATTGTGAAAAAATAATTTATAAATATTTGTTTACATAAACAACATAGTAATGTAA AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTAGTG <u>AATCTAATTTAATATTATTGATATTATGATTTTACGTTTCTCGTTCAGCTTTCTTGTA</u> 1741 ATAATAGTAATTCTAGCTGGTTTGATGAATTAAATATCAATGATAAAATACTATAGAAAA GATITICCGCTITICCAGCGTTCGGCACGCACGACGACGACGGCTTCATTCTGCATGGTTGTGC AACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATACTTCGGGTAGTG CCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACAGGGAC ccancaacercrearrireeceaaaarrigeeceaggerreecegrareacaggae TGCGTCGGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTT TGCGTCGGGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTT GATTCATAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTTATGCAA GATTCATAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTTATGCAA AATCTAATTTAATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTCTTGTA CAAAGTGGTCTCGAAGTTCGGTACCCCAGCTTGGTAAGGAAATAATTATTTTCTTTTT 1681 ITTTAATGAATTTGATCGAACATGTAAGATGATATACTAGCATTAATATTTGTTTTAATC TCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCT TTACCAGACCGGAGATATTGACATCATATATGCCTTGAGGCAACTGATAGCTGTCGCTGTC ACGATAACGGCTCTCTCTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGT Accamaccccrcrcrrrranacccraaaccrraaacrcrccrcrr TCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCT GATITICCGCTTTCCAGCGTTCGGCACGCACGACGGCTTCATTCTGCATGGTTGTGC TTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTC 1801 1441 1561 1621 1501 1081 1141 14140 1261 14260 1321 14320 1381 14380 14440 1021 961 14080 1201 781 13780 841 13840 901 13900 13960 14020 g g à 엄 ð ð 8 8 Ωp ð g  $\dot{\delta}$ g ò ద  $\dot{\delta}$ g à g δ Op  $\delta$ g 중 유 ò g 8 6 δ д ð ò g à

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA.

Claim 13; Page 62-72; 104pp; English.

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Helliwell

Waterhouse P,

Wesley S,

WPI; 2002-682669/73.

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The present invention describes a vector (1) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a cecipient cell, preferably in bacteria such as Bacherichia coll; (b) selectable marker region capable of being expressed in the recipient cell cand (c) a chimeric DNA construct comprising: (i) promoter or promoter region dapable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and collydealylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites, or the second and third recombination sites, or the second in the complimation sites or the third and fourth recombination sites, do not recombination site, or the third and control fourth recombination sites, may be used for silencing large amounts of double-stranded RNA which can be used for silencing target nucleic cald sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention of the phenotypic expression of nucleotide chimeric gene for reduction of the phenotypic expression of nucleotide sequence from the present invention

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                                                                                                                                                                                                                             ABQ82130 standard; DNA; 18691 BP.
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2001US-0333743P.
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WO200259294-A1.

Synthetic

01-AUG-2002

11-DEC-2002

ABQ82130;

26-JAN-2001; 29-NOV-2001;

13240

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13180

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Gaps

Indels 1121;

Length 18691; T; 0 U; 0 Other;

DB 6; 22;

72.3%; Score 3234.8; 79.5%; Pred. No. 0; Pred. No. 0; 0; Mismatches

Matches 4429; Conservative

Local Similarity

Query Match

Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626

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New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for replication, a selectable marker and a chimeric DNA construct, useful for replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-region to the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the present invention sites, do not recombination sites, or the third and same recombination sites, do not recombine with each other or with a same recombination site, and preferry of the present invention can be used for silencing target nucleic confidering of the present invention of the phenotypic expression of nucleic confidering of the present invention of the phenotypic expression of nucleic sequence from the present invention of the phenotypic expression of nucleic sequence from the present invention of the phenotypic expression of nucleic sequence consulation.

So equence 17488 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;

Q Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
Query Match
Best Local Similarity 62.4%; Pred. No. 4.5e-173;
Matches 2321; Conservative 0; Mismatches 1312; Indels 86; Gaps 17;

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ATGTCAAAAAGAGGTGTATTGAAGCAGCGTATTACAGTGACAGTGACAGCGACA 16210  ACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGT 560  GCTATCAGTTGCTCAAGGCATATTGTATGTCAATTTCTCCGGTCTGGTAAGCACAACCAT 16150  GTATAAGGAAGCACATTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGT 620  GTATAAGGAACCCGTCGTCGGTGCCGAACGCTGGAAAAATCAGGAAAGG 16093  CATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAAAATCAGGAAAGGG 680  GTTTTTCGCGGGTGGTTATTGAAATGAAAGGCTTTTTCGCTGAAGAACAGGG- 16034  GATTGTCGCGGGTGCCCCGCTTCTTCCCCGATAACGGAAAAACGGGG- 16034	CCATATCGGTGGTCATCATCGCCGGATATGCACCGGGGTAAGTT 740 ACTGGTGAAATGCAGTTTAAGGTTTACACCTATAAAAGAGAGGCGGTTATCGTC 15979  CACGGGGAGACTTTATCTGACAGCGGACGTGGCCGGGGGGATCGCTCGTCGCC 800  TGTTTGTGGATGACATCATTATTGACACGCGGGGGGATCGTCACTCTCTT 860  TGTTTGTGAATGATATATCACTCTGTACATTATTGACAGGGGATCGTCACTCTCTTT 860  CGGGCGTGTCAATAATATCACTCTGTACATCCCGCGGGGACGGATGGTGATCCCC 15919  CGGGCGTGTCAATAATAACTCTCAGATAACTCTCCCGTGAAACTCTCCTCTTT 860  TATAGGTGTAAACTGCATTCACACCCGGAAAACTCTCCTGTTCTCGCTATA 15859  TATAGGTGTAAAACTGCAATACACCACCGGTATGGCCGGTTCCGTTA 15799  GGCCGTTCATTCAATAAACTGGCCACCCGGAAATGACCCTTCCTGATTTCCGCTTT 974  TCGGGGAAGAAGACTCGCTCACCCGGCGCCCCCCGGTTCCTTCC	CAGCGTTCGGCACGCAGACGACGGCTTCATTCTGCATGCTTGCAGACCG 1031	TTTATTTTTTTTTTCGGAAGTGATCTTCGGCGGAAGTGCGTCG 15448  GGTGATGCTGCCAACTTAGTCGACTACACGGATTTTTTTT
16266 AIGTCAAAAGAGGGTGTGCTATGAA- 501 ACTTACTAAACGTGATAAAGTTTCTC 16209 GCTATCAGTTGCTCAAGGCATTATATT 561 GTATAAGGAGCCTGACATTATATT 16149 GCAGAATGAAGCCCGTCGTCTGCGTC 621 CATTTTCGCGGTGGCTGAGATCAGCC 16092 GATGGCTGAGGTCGCCCGTTTATT	681 CCATATCGGTGGTCATCG 16033ACTGGTGAAATG 741 CACGGGAGACTTTATCTC 15978 TGTTTGTGGATGTACAG 801 CGGCGTGTCAATAATA) 15918 TGGCGTGTGAATAATA 15918 TGGCGGTGTAAACTTGAG 861 TATAGGTGTAAACCTTAG 15858 TCGGGGATGAAGCTGGG 915 GAGCCGTTCAATTCAATY 15798 TCGGGGAAGAAGTGGCTC 15798 TCGGGGAAGAAGTGGCTC 15798 TCGGGGAAGAAGTGGCTC 15798 TCGGGGAAGAAGTGGCTC	975 CAGCGTTCGGCACGG 15738 TGATGTTCGGGGATA 1032 GAGATATTGACATCATA 1052 TAATACGCTGCTTCATA 1092 TAATACGCTGCTTCATA 1148 ACGTCTCATTTCGCCA 11567 ACGTCTATTTCGCCA 11567 ACGTCTCATTTCGCCA 1168 ACGTCTCATTTTCGCCA 1168 TTTATTTTCGCCA	15507 TTTATTATTCTGGGAACTT. 1268 GGTGATGCTGCCAACTT. 1328 AGTGACTGCTGCCAACTT. 1338 AGTGACTGGATATGTTG 1388 TTTAATATATTGATATT 1388 TTTAATATATTGATATT 15327 TTTAATATATTGATATT 15267 GTCTGGAGGAATTCGGT 15267 GTCTCGAGGAATTCGGT 15267 GTCTGGAGGAATTCGGT 15267 GTCTGGAGGAATTCGGT 15267 GTCTGGAGGAATTCGGT 1521 ATGATAAAATAGTTAAG

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1568 GIGAAAAATAATITIAIAAATATITITIACATAAACAACATAGTAATGTAAAAAATA 1627 
1628 TGACAAGTGATGTGTAAGACGAAGATAAAAGTTGAGAGTAAGTTATTTTTAAT 1687 
1688 GAATITGAICGAACAIGFAAGAIATACIAGCAITAATATITGITITAAICAIAATAG 1747 15031 TAGCAITAGAITAIGITITGITACAITAGAITACIGITICIAITAGITITGAIATTAGI 14972
1748 TAATICTRGCIGGITITGAAGAATTAAATAICAATGATAAAAAAAATAAGA 1807 14971 TIACTTIAGCITGITAITIAATATITIGITIAATAAAATAA
1808 ATAAATAAATTAAAATAATTITTTTTATGATTAATAGTTTATTATATAATTAAATTGT 1867 14911 CTAACAAAATATTTATTAACTTTTAAACTAAAATATTTAGTAATGGTATAGATATTAAT 14852
1868 ATACCATTACTAAATATTTTAGTTTAAAAGTTAATAATATTTTGTTAGAAATTCCAATC 1927 14851 TATATAATAACTATTAATCATAAAAAAATATTATTATATTTTTATTTTATTTTTA 14792
1928 IGCTIGIBALTTAICAATAACAAAATATTAAATAACAAGCTBAGTAACAATAATAT (1987) 14791 CTATAGTATTTAICATTGATATTTAATTCATCAACCAGCTAGAATTACTATTAIGATT 14732
1988 AAACTAATAGAAACAGTAATCTAATGTAACAAAACATAATCTAATGCTAATATAACAAAG 2047 14731 AAAACAAATATTAATGCTAGTATATCATCTTACATGTTCGATCAAATTCATTAAAAATAA 14672
2048 GGCAAGAICIAICAITITAIAIAGIAITAITITICAATGACAITCITATIAAITICIAAA 2107 14671 TAIACITACTCICAACTITIAICITCITCGICITACACATCACTIGICAIAITITIAC 14612
2108 TAATACTTGIAGTTITATTAACTTCTAAATGGATTGACTATTAATTAAATGAATTAGTCG 2167 14611 ATTACTATGTTATGTAAACAATATTATATAAATTATTTTTCACAATTATATAACAATTATT
2168 AACATGAATAAACAAGGTAACATGATAGATCATGTGTTGTGTTATCATTGATCTTACAT 2227
2228 TIGGATIGATIACAGTIGGGAAGCIGGGTICGAATCGAIAAGCTIGGAICCICIAGACC 2287
2348 TAGAITITGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTCACTA 2407 
2408 TGAATCAACTACTTAGAIGGTATTAGTGACCTGTAGTCGACTAAGTTGGCAGCATCACC 2467 
2468 GACGCACITIGCGCCGAAIAAATACCIGIGACGCAAGAICACTICGCAGAAIAAATAAAT 2527 
2528 CCTGGTGTCCCTGTTGATACCGGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTT 2587 14205 CCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAAATGAGAGGTT 14146
2588 GALCGGALTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGGATTT 2647 14145 GATCGGCACTACCGAAGTATGTCAAAAAGAGGTGTGCTATGAAGCAGCGTATTAC 14090

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                                  4089 AGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCC 14030
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                                                                         CTGTGTATAAGGGAGCCTGACATTTATATTCCCCAGAACATCAG
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TCAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAATTTTCTACTGTATCGACCTGC
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bacherichia coll; (b) selectable marker region capable of being expressed in the recipient cell c; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites, (iii) 3' transcription terminating and courth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and same recombination sites, do not recombination site, and preferably are same recombination sites, do not recombination site, or the third and same recombination sites and second recombination site or with each other or with a same recombination site.

Of double-stranded RNA which can be used for silencing target nucleic and sequences. The vectors can also be used to convert a DNA fragment from a silence of second silence of some and second second with a same recombination site of some silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of second silence of seco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA fragments having an origin of
chimeric DNA construct, useful for
producing large amounts of double-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to gene for reduction of the phenotypic expression of nucleic. The present sequence represents an acceptor vector nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         into an inverted repeat structure. Plants transformed with a vector the present invention can be used in a conventional breeding scheme produce more plants with the same characteristics or to introduce a
                                                                                                                                                                                                                           l cloning; silencing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric gene for reduction of the phenotypic expression of nuclei
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                                                                                                                                                                          Acceptor vector pHELLSGATE 8 nucleotide sequence SEQ ID NO:24
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Pred. No. 2.1e-172;
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                                                                                                                                                                                                                              Chimeric nucleic acid construct, recombinational recombination site; double stranded RNA; plant; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New vectors comprising operably linked replication, a selectable marker and a silencing target nucleic acids and for
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recgaagte           recgaagte	CAACTTAGE	ATGTTGTG:          ATGTTGTG	SATATTTA'          SATATTTA'	rrcggrace   ccaagcrra	GTATAAAA      TGATAACA	TGAAAAA         TTAATTAA	GACAAGTG       TAAGAATG	AATTTGAT   	AATTCTAG 	TAAATAAA         TAACAAAA	TACCATTA      ATATAATA	GCTTGTAA         TATAGTAT	aactaata       aaacaaat	GCAAGATC         	AATACTTG    TTACTATG	ACATGAAT    TATATTAT	TGGATTGA 	CTTTGTAC
TTTATTTATTC:            TTTATTTATTC:	GGTGATGCTGC	SACTGGATA          SACTGGATA	TTTAATATATTGATATTTATAT( 	ctcgaggaattcggtacco                ctagaggatccaagcttat	TCCTTTTA         AAGATCAA	TATAATTG    TAATTCAT	AAAAATAT        GAAATTAA	TTTTAATG       GTTATATT	ATAATAGT         TTATTTGT	aataagaa   Ggaatttc	AATATCTA 	TCCAATCT   PATTTTAC	TAATATCA             TATGATTA	DAACAAAGC	TTCTAAAI         TTTTTACA	ATTAGTCGA    FATAACAAC	CTTACATT     AGGAAAAA	rctagacca
			8 TTT 	8 GTC	8 TTT     5 TGT	8 TGT 5 GAC	8 TAA     S TTA	B TAT	8 ATC	8 AAA   5 ATT	യഥ	ω ω	8 AAA 	8 TAT   5 TT2	8 AA7     5 AT7	8 GAA	8 GA7	B CC
1208	1268	1328	1388	1448	1498	1558	1618	1676	1738	1798	185	191	197	203	209	215	221	

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13388 GAATAGGTAGATGTTTTTTTTTTTTCACACAAAAAAGAGGCTCGCACCTCTTTTTTCTTAT 13329
                                                                                                  TICTITITATGATITAATACGGCATIGAGGACAATAGCGAGTAGGCTGGATACGACGATT 13269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                        ATTTAATATATTTATATATATCATTTTACGTTTCTCGTTCAGCTTTTTTGTACAAACT
                                                                                                                                              CCGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAAG
                                                                                                                                                                                             ccertricacadacatritecadecrerecerceactaactreccaccarcacceada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
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attP2,

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comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. [1], [11], [11], primers, vectors and methods att recombination site. [1], [11], primers, vectors and methods att recombination site. [1], [11], primers, vectors and methods curve to intracellular locations, cleaving fusion tays from gene products to intracellular locations, cleaving fusion tays from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. [1], [11], [11], host cells and vectors can be used in the production of polypeptides and antibodiaes. The present sequence is used in the exemplification of the present invention
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Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;

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100	0; Ga	E 4
Length 4	Indels	
DB 3;	149;	
24.8%; Score 1108.8; DB 3; Length 4470;	99.8%; Pred. No. 5.1e-149; tive 0; Mismatches 2; Indels 0; Gaps 0;	
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ABZ58767 standard; DNA; 4470 ABZ58767; RESULT 8 ABZ58767 

145

BP.

Destination plasmid pDONR201 nucleotide sequence.

(first entry)

01-MAY-2003

Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; ds.

Synthetic.

325 401 385 461 445 521 505 581 565 641

WO200295055-A2.

28-NOV-2002.

21-MAY-2002; 2002WO-US015947.

21-MAY-2001; 2001US-0291973P.

(INVI-) INVITROGEN CORP.

Byrd Esposito D, × Ë Cheo D, Brasch MA,

WPI; 2003-129436/12.

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.

Disclosure; Fig 26B-C; 273pp; English.

625

701

685

745

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence

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               4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;
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Pred. No. 5.1e-149;
0; Mismatches 2;
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1062 ACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC 1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site-specsific recombination; array construction; reporter gene fusion; mutagenesis; protein production; protein characterisation; plasmid pMK2010; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moving an insert nucleic acid between vectors using site-specific recombination in vivo, useful for studying the biology of the organism, including array construction, reporter gene fusions, mutagenesis and protein production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises a method for moving an insert nucleic acid molecule between vectors, the method involves moving an insert nucleic acid from one vector to another using site-specific recombination. The method of the invention is useful for studying the biology of an organism, including array construction, reporter gene fusions, mutagenesis, protein production and characterisation. The present DNA sequence represents the plasmid vector pMK2010 of the invention.
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                                                                                                                      ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC
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conciding an attB1, attB2, attB1, attB2, attB1, and attB2 nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide combination sites and (2) an isolated nucleic acid molecule (III) remorphishing at the recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated at recombination sites comprising at least one mutation between a first nucleic acid molecule comprising one or more mutated at recombination site and a second nucleic acid molecule comprising at ecombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second nucleic acid molecules for the recombination of the present invention are used for the recombinational cloning of act recombination are used for the recombinational cloning of act molecules of intracellular locations, cleaving fusion tags from central proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing replicons, cloning into phages and cloning (1), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3696 AATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTC 3755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding an attB1, attB2, attB2, attL1, attL2, attL2, attR1 nucleotide sequence useful for the recombinational cloning of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3636 GCCAACTITGTACAAAAAGCTGAACGAGAACGTAAAATGATATAAATATCAATATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage lambda; att; recombination site; attB; attR; at mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes isolated nucleic acid molecules (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.8%; Score 1108.8; DB 3; Length 4939; ilarity 99.8%; Pred. No. 5.1e-149; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 U; 0 Other;
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                    Donor plasmid pDONR205 nucleotide sequence.
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99US-0126049P.
99US-0136744P.
                                                                                                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                 02-MAR-2000; 2000WO-US005432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brasch MA,
                                                                                                                                              Bacteriophage lambda
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Matches 1110; Conserv
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RESULT 11
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comprising one or more mutated att recombination sites comprising at least one mutated att recombination sites; and (2) an isolated mucleic acid molecula (III) comprising one or more mutated att recombination sites comprising at least one mutated att recombination in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (III), (III), primers, vectors and methods attrement invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting generated proteins, operably linking mucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attB2, attB1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its ore region that increases the specificity of interaction between the recombination site and a second att
                                                              Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population, (c) mixing the second population of all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules of the second population to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules.
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                                                                                                                                                                                    The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, comprising one or more recombination sites with a target the first population to recombine with the first target nucleic acid molecules of nucleic acid molecules of nucleic acid molecules of nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR212 nucleotide sequence
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                                                                                Inserting a population of nucleic acids into a second target selecting and isolating nucleic acid molecules by mixing the population of nucleic acid with a second target nucleic acid.
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the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR212(F) nucleotide sequence
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larity 99.5%; Pred. No. 4.1e-148;
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                                                   TTCAATAAACGGGGGGACTCAGCCATCCTTCTTGATTTTCCGCTTTCCAGCGTTCGGC
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                                                                                               ACGCAGACGACGGCCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC
                                                                                                                                                         ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC
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Sequence 21,

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Sequence 5, App. Sequence 9, App. Sequence 13, A Sequence 13, A Sequence 13, A Sequence 21, A Sequence 2, App. Sequence 2, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 1, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 2, App. Sequence 3, App. Sequence 3, App. Sequence 3, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, App. Sequence 4, Ap

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Sequence 24, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
APPLICANT: Helliwell, Christopher A.
APPLICANT: Helliwell, Christopher A.
APPLICANT: Helliwell, Christopher A.
APPLICANT: Helliwell, Christopher A.
APPLICANT: Materhouse, Peter
APPLICANT: Helliwell, Christopher A.
APPLICANT: Helliwell, Christopher A.
APPLICANT: Hellide Constructs
TITLE OF INVENTION: Using recombinational cloning
FILE REPERSENCE: HELLGA
FILE REPERSENCE: HELLGA
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PetentIn version 3.1
SEQ ID NO 24.26
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity 100.
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121 ACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATTAGTGACC

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Db 13120 ACTGTAAAACACATATCCAGTCACTATGAATCAACTAGATGGTATTAGTGACC 13  Qy 181 TGTAGTCGACCGACAGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTGACCG 24  Db 13180 TGTAGTCGACGGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCG 13  Qy 241 ACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTATTGTC 30  13240 ACAGCCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTATTGTC 30  Qy 301 CTCAATGCCGTATTAAAACAAAAAAAAAAAAAAAAAAAA	361 13360 421 13420	134 88 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	13350 601 13600 661	121 ATGCACCACCGGGTAAAGTTCACCGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAG	Oy         841 ACGATAACGGTCTCTCTTTTATAGGTGTAAACCTTAAACTTTCACCAGTCCCTGT         900           Db         13840 ACGATAACGGTCTCTTTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGT         138           Oy         901 TCTCGTCAGCAAAAAGCCGTTCATTTCAATAAACCGGGGGGACCTCAGCCATCCT         960           Db         13900 TCTCGTCAGCAAAAAAGCCGTTCATTTCAATAAACCGGGGGACCTCAGCCATCCTTCCT	961	OY 1021 TTACCAGACGGAGATATTGACATCATATAGCCTTGAGCAACTGATAGCTGTC 1080  14020 TTACCAGACGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTC 1407.  OY 1081 AACTGTCACTGTAATACGCTGCTTCATAGCACCTCTTTTTGACATACTTCGGGTAGTG 1140  Db 14080 AACTGTCACTGTAATACGCTGCTTCATAGCACCTCTTTTTGACATACTTCGGGTAGTG 1140  14080 AACTGTCACTGTAATACGCTGCTTCATAGCACCTCTTTTTGACATACTTCGGGTAGTG 1141	00
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APPLICANT: Weeley, Susan V.
APPLICANT: Weeley, Susan V.
APPLICANT: Weeley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Using recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
SUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
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US-10-055-001A-26
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95.6%; Pred. No. 0;
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; Sequence 26, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial sequence
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Matches 4477; Conservative
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13181 AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACACAACATATCCAGTC 13240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: octopine synthase gene terminator region
                                                                      NAME/KEY: misc feature
LOCATION: (16551)..(16319)
OTHER INFORMATION: attP2 recombination site (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (13675)..(13980)
OTHER_INFORMATION: cddB selection marker (complement)
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ON: (17610)..(16855)
INFORMATION: ccdB selection marker (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (2149)...(2706)
OTHER INFORMATION: a left T-DNA border region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.3%; Score 3234.8;
79.5%; Pred. No. 0;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (13048)..(13279)
OTHER INFORMATION: attP1 recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (497). (1442)
OTHER INFORMATION: nptl1 coding region
                                                                                                                                               FEATURE:
NAME/KEX: misc_feature
LOCATION: (14660)..(16558)
OTHER INFORMATION: pdk2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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LOCATION: (17922)..(18)
OTHER INFORMATION: oct
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LOCATION: (264)..(496)
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Matches 4429; Conserv
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US-10-055-001A-13
Sequence 13, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION
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APPLICANT: Wesley, Susan V.
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CURRENT APPLICANTON WUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 13.
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                                                                         17441 AAAAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTAC 17500
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                                                                                                                                                                                                                                                                                                                              CACCATTCAACCCGGTCCAGCACGCCGGGTAACCGACTTGCTGCCCGAGAATTAT 4295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCTGCAGGCATGCAAGCTTAGTTAGTAGTGATGCATATTCTATAGTGTCACCTAAATCT
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                               AAAAGACTGATTACATAAATCTTATTCAAAATTTCAAAAGGCCCCCAGGGGCTAGTATCTAC
                                                                                                                               GACACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCCGCCGGCG
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LOCATION: (17890)..(17659)
OTHER INFORMATION: attP1 recombination site (complement)
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NAME/KEY: misc_feature
LOCATION: (10706)..(11324)
OTHER INFORMATION: right T-DNA border fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: acceptor vector PHELLSGATE
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NAME/KEY: misc_feature
LOCATION: (11674)..(13019)
OTHER INFORMATION: CaMV35S promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (7922)..(9985)
OTHER INFORMATION: spectinomycin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial sequence
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8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6	0 0 0 0 0
13421 AGRAMIAAGRAMAGAGGCCGGCCTCTTTTTGTCGCCCAAATTAAAAACATCTCTTTTTGTCGCCCAAAATTAAAAACATCTCCTTTTTTGTCGCCCAAAATTAAAAACATCTCCTTTTTTTGTCGCCCCAAAATTAAAAACATTCCCACTTTTTTGTCGCCCCAAAATTAACATTTCCCACTTTTCTTTTTTTT	DD 14141 AIATTAGCCTTGAGCAACTGATGCTGTCAACTGTCATATAGCTGCTTC 14200  1106 ATAGCACACCTCTTTTGACATACTTCGGTAGTGCCGATCACGTAATACGCTGCTT 1165  14201 ATAGCACACCTCTTTTTGACATACTTCGGGTAGTGCCGATCAACGTCTCTTTTTCGCCAA 14260  OY 1166 AAGTTGGCCCAGGGCTTCCCGGTAGTGCCGATCAACGTCATTTTCGCCAA 14260  DD 14261 AAGTTGGCCCAGGGCTTCCCGGTACTCACGGATTTATTTA

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                                                                                                                                              Score 1277.8; DB 15; Lengt
Pred. No. 1e-183;
0; Mismatches 1312; Indels
                                                                                                 ; OTHER INFORMATION: acceptor vector PHELLSGATE11 US-10-055-001A-25
 OF SEQ ID NOS: 26
RE: PatentIn version 3.1
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ilarity 62.4%;
Conservative
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NUMBER OF SEQ II
SOFTWARE: Patent
SEQ ID NO 25
LENGTH: 17458
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US-10-055-001A-25/c
US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Sequence 25, Application US/20030049835A1
; GENERAL INFORMATION:
; APPLICANT: Waterhouse, Peter
; APPLICANT: Waterhouse, Peter
; APPLICANT: Helliwell,Christopher A.
TITLE OF INVENTION: Wathod and means for producing efficient silencing constructs
; TITLE OF INVENTION: using recombinational cloning
; FILE REFERENCE: HELLGA
; CURRENT APPLICATION NUMBER: US/10/055,001A
; CURRENT FILING DATE: 2002-06-11
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Sublication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Wethod and means for producing eff.;
TITLE OF INVENTION: using recombinational cloning;
FILE REFERENCE: HELICA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
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llarity 62.1%; Pred. No. 5.5e-183;
Conservative 0; Mismatches 1325;
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ORGANISM: Artificial sequence
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Best Local Similarity
Matches 2316; Conserv
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US-10-055-001A-24/c
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3337 GAATAGGTAGATGTTTTTATTTTGCACACAAAAAGGGCTCGCACCTCTTTTCTTAT 3396 	දුරු පු	261 CTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCA 320 
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3457 CCGTTTGAGAAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAAG 3516	oy Oy	381 TACCTATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTC 440 
3517 AACATTTGGAAGGCTGTCGGCGGCTCACTAATACCATCTAAGTAGTTGATTCA 3576	Qy Db	441 ACAACTCTTATACTTTTCTTTACAAGTCGTTCGGCTTCTTCTGGATTTTCAGCCTCTT 500 16284 ATGTCAAAAAGAGGTGTGTTATGAAGCAGCGTATTACAGTGACAGTTGACAGCGACA 16228
3577 TAGTGACTGGATATGTTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTA 3636 	oy Db	501 ACTIACTAAACGIGATAAAGTITCTGTAATTICTACTGTATCGACCTGCAGACTGGCTGT 560 16227 GCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAACCAT 16168
3637 ATTTAANATATTGTATTATATCATTTTACGTTTCTCGTTCAGCTTTTTTGTACAAACT 3696 	oy Op	561 GTATAAGGGAGCCTGACATITATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGT 620
3697 TGTCTAGAG 3705 	y dg	621 CATITICGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGG 680 16110 GATGGCTGAGGTCGCCCGGTTTATTGAAATGAACGGCTCTTTTGCTGACGAGAACAGGG- 16052
RESULT 9 10-388-546-7/C	Sy da	
Sequence ', Aprica 100 05/10055310 Publication No. US20030175783A1 GRNERAL INFORMATION: APPLICANT: Waterhouse, Peter	\$ A	741 CACGGGAGACTITATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCGTCGCC 800  15996 TGTTTGTGGATGTACAGAGTGATATTATTGACACGCCGGGCGACGGATGGTGATGCTCCCC 15937
APPLICANT: Wesley, Susan APPLICANT: Helliwell, Chris TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing FILE REPERENCE: COLINA-US2	çy qo	801 CGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTT 860
CURRENT APPLICATION NUMBER: US/10/385,546  CURRENT FILING DATE: 2003-03-12  PRIOR APPLICATION NUMBER: US 60363852  PRIOR FILING DATE: 2003-03-14	상 음	861 TATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAA 914
R OF SEQ ID M ARE: Patentin NO 7 TH: 17476	λό qα	915 GAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTTTCCGCTTTC 974 15816 TCGGGGAAGAGGGTGATCTCAGCCACCGCGAAAATGACATCAAAACGCCATTAACC 15757
TYPE: DNA ORGANISM: Artificial FEATURE: OTHER INFORMATION: plasmid pHELLSGAIE 8	े ठे वे	975 CAGCGTTCGGCACGAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACCG 1031
-546-7 atch 28.4%; Scc	λο O	1032 GAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCACTG 1091
6; Conservative 0; Mismatches 1325; Indels 88; Gaps CTCGAGACATTTGTACAAAAAGCTGAACGAAAACGTAAAAAGATGATTATAAATATCAAT	QY Dp	
	S da	1148 ACGICTCATITICGCCAAAAGIIGGCCCAGGGCTICCCGGIAICAACAGGGACACCAGGA 1207 
ATATTAAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATC CAGTCACTATGAATCAACTGACTGAGTGATTTAGTGACCTGTAGTCGACCGAC	QY	1208 TITATITATICOGGGAAGIGATCITICCGTCACAGGTATITATICGGGGCAAAGIGCGTCG 1267 
16584 CAGTCACTATGAATCAACTAGTAATGGTATTAGTGACCTGTAGTCGACGACAGCCTT 16525 201 CCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGAC	δ	1268 GGTGATGCTGCCAACTTAGTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCAT 1327

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15406 1387 15346 1447 1528 1522 1557	TGTAAGATCAAGGATGACAAGAACTAATCATCATCATGTTATTTAT	TTAAATATCTATACCATTACTAAATATTTTAGTTAAAAGTTAATAAATA	AATTTCTAAATAATACTTGTAGTTTTATTAACTTCTAAATGGATTGACTATTAAAAT 2157
= ',	15225 TGTAAGATCAATGA' 1558 TGTTATAATTGTGA' 15165 GACTAATTCATTTA' 1618 TAAAAAATTAATAA' 15105 TTAGAAATTAATAA' 1678 TATTTTTAATGAAT' 15045 TTTGTTATTAATGAAT' 1738 ATCATAATAGTAAT' 1738 ATCATAATAGTAAT' 1738 ATCATAATAGTAAT' 1798 AAAATAAGAATAT	1858 TTAAATATCTATAC 14865 GATATTTAATTATA 1918 AATTCCAATCTGCT 14805 CTTATTTTTACTAT 1978 AAATAATTAAAA 2038 TATAACAAAGCGCA 2038 TATAACAAATAAATA	2098 AATTCTAAATAAT 14625 ATTTTTTTACATTA 2158 GAATTAGTGGAACA 14565 ATTATACAACTATG 2218 GATCTTACATTTG 2218 GATCTTACATTTG 2218 GATCTTACATTTG 14505 AAAGGAAAAAAGAA 2278 CCTCTAGACCACTT 2338 TATATTAAATTAG3 14395 TATATTAAATTAG3 14395 TATATTAAATTAG3

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2518	ADAATAAATCCTGGTGTCCCTGTTGATACCGGGAAGCCCTGGGCCAACTTTTGGCGAAA 2577 
2578	ANGAGACGITGANCGGANITICACAACTCITATACITITCTTACAAGTCGITCGGCITC 2637 
2638	atctggattttcagcctctatacttactaaacgtgataagtttctgtaat 
2698	ATCGACCTGCAGACTGGCTGTGTATAAGGGAGCCTGACATTTATATTCCC 2748 CAATATCTCCGGTCTGGTAAGCACATGCAGAATGAAGCCCGTCGTCGTCTGCGTGCC- 13982
2749	AGAACATCAGGTTAATGGGGTTTTTGATGTCATTTTCGGGGTGGGT
2809	CTTCCCGAATAACGGAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTT 2868
2869	CATCCCCGATATGCACCACCGGGTAAAGTTCA 
2929	CACTGGCCAGGGGATCACCATCCGTCGCCGGGGTGTCAATAATATCACTCTGTACAT 2988 ACACGCCGGGCGACGGATGGTGATCCCCTGGCCAGTGCACGTCTGCTGTCAGATAAAG 13749
2989	CCAC     TCTC
3049	CAGTCCCTGTTCTGGTCAGGAAAAGAGCCGTTCATTCAATAAACC
3103	TCAGCCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGCACGACGACGACGACGGCT 3159
3160	TCATTCTGCATGGTTGTGCTTACCAGACGAGATATTGACATCATATATGCCTTGA 3216
3217	GCAJ TTA
3277	7 TITIGACATACTICCGTICTIGATGCAGATGATITICAGGACTATGACACTAGCGTATAT 3336
3337 13386	7 GAATAGGTAGATGTTTTTTTTTTTGTCACAGAAAAAGAGGCTCGCACCTCTTTTCTTAT 3396 
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LOCATION: (3495)(4134)  THER INFORMATION: ori 0-151-690-21  24.8%; Score 1108.8; DB	t Local S ches 1110	Qy 26 GACAAGTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATATTT 85	QY 86 AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAACACAACATATCCAGTC 145 Db 162 AAATTAGATTTTGCATAAAAACAGACTACATAATACTGTAAAAACACAACATATCCAGTC 221	QY 146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACCGAC	Qy 206 IGTICTICGGGIGAIGCTGCCAACTIAGTCGACGGCCTTCCAAAIGTICTICTGAA 265	Qy 266 ACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAA 325	OY 326 AGRARIAAGAAAAAGAGGTGCGAGCCTCTTTTTGTGTGACAAAATAAAACATCTACCT 385	QY 386 ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC 445	QY 446 TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 505	OY 506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 565	Qy 566 AGGGAGCCIGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 625	QY 626 TGGGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 685	QY 686 TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACGGGTAAAGTTCACGG 745	QY 746 GAGACTITATCTGACAGCAGACGTGCACTGGCCAGGGGATCACCATCCGTCGCCCGGGC 805	QY 806 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTTTTTATAG 865	QY 866 GTGTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCAT 925	Qy 926 TTCAATAAACGGGGGACCTCAGCCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGC 985	ACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC 1
OY 3457 CCGTTTGAGAACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAAG 3516  Db 13268 CCGTTTGAGAAGAACATTTGGAAGGCTGTCGACTAAGTTGGCAGCATCACCCGAAG 13209  OY 3517 AACAȚTTGGAAGGCTGTCGACTACATACATACTAAGTTGATTCA 3576		Qy 3577 TAGTGACTGGATATGTTGTGTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTA 3636  Db 13148 TAGTGACTGGATATGTGTTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTA 13089	OY 3637 ATTTAATATATATATATATATATATACATTTACGTTTCTCGGTGAGCTTTTTGTACAAACT 3696  13088 ATTTAATATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTTTGTACAACT 13029	OY 3697 TGTCTAGAG 3705 Db 13028 TGTCTCGAG 13020	RESULT 10 US-10-151-690-21 : Seminore 21 Annlication US/10151690	; Publication No. 0220030124555A1 ; GENERAL INFORMATION: ; APPLICANT: BRASCH, MICHAEL A. ; APPLICANT: CHEO, DAVID	מיני הייומים על אמושגימת או סמו ממס מתמשמ	FOR OSE IN ISOLATION OF	FRIOR FILING DATE: 2002-05-21 FRIOR FILING DATE: 2001-05-21 FRIOR FILING DATE: 2001-05-21 NUMBER OF SEO IN NOW. 64	; SOFTWARE: Patentin Version 3.1 ; SEQ ID NO 21 ; LENGTH: 44.70 ; TYPR: NNA	GRGANISM: Artificial sequence FEATURE: OTHER INFORMATION: plasmid pDONR201	NAME/KEY: gene LOCATION: (29)(260) OTHER INFORMATION: attPl	NAME/KEY: gene LOCATION: (656)(961) OTHER INFORMATION: ccdB	NAME/KEY: gene LOCATION: (1099)(1184) OTHER INFORMATION: ccdA	) NAME/KEY: gene ; LOCATION: (1303)(1962) ; OTHER INFORMATION: CmR	NAME/KEY: gene COCATION: (2210)(2442) COTHER INFORMATION: attP2	; NAME/KEY: gene ; LOCATION: (2565)(3374) ; OTHER INFORMATION: Kmr	; FEATURE: ; NAWE/KEY: gene

AAATATCAATA AAATATCAATA ACAACATATCC            caacaacatatcc	2 ACHTGAATCAACTACTTAGATGATTAGTGACCTGTAGTGACCGACGACCCTTCCAAA 5 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGACGACGACCTTCCAAA 6 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACGACGACGTCCTAAATGTTCTTCTCAA 7 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACGCCTTCCAAATGTTCTTCTCAA 7 TGTTCTTCGGGTGATGCTGCCCAACTTAGTCGACCGACGCCTTCCAAATGTTCTTCTCAA	266 AGGGAATCGTGTATCCAGCCTACTGCCCTATGTCCTCAATGCCGTATTAAATCATAAAA 325	4 N N	522 TCTIATACTITCTCTACAAGTCGTTCGGCTTCATCTGGATTTTCACCCTCTACTTA 581 506 CTAAACGTGATAAAGTTCTTCTATTTCTACTATCACCTGCAGACTGGCTGG		626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 685	686 TCGGTGGTCATCATGCGCCAGGTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGG 745 	746 GAGACTTTATCTGACAGCGAGACGTGCACTGGCCAGGGGGATCACCATCGGTCGCCCGGGC 805	806 GIGICAALAATALCACTCIGTACATCCACAAACAGACGATAACGGCTCTCTTTTATAG 865	866 GIGTAAACCTIAAACIGCAITTCACCAGICCCIGTICICGICAGCAAAAGAGCGGTICAI 925	926 TICAAIAAACCGGGCGACCICCAGCCAICCCTICCTGAITITCCGCTTICCAGCGTICGGC 985	986 ACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC 1045	1046 ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCATGTAATACGCTGCTTC 1105 
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	RESULT 11 US-10-357-268-1 ; Sequence 1, Application US/10357268 ; Publication No. US20030219902A1 ; Roblication No. Wichell	APPLICANT: Rann, Michael L APPLICANT: House, Brent L APPLICANT: House, Brent L TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination FILE REFERENCE: WSUR-1-20291 CURRENT APPLICATION NUMBER: US/10/357,268 CURRENT FILING DATE: 2003-01-31	FALOR FILLING DATE: 2002-01-31 NUMBER OF SEQ ID NOS: 5 SOFTWARE: Patentin version 3.2 ENGIN NO 1 LENGTH: 4892 TYPE: DNA	ORGANISM: Escherichia coli FEATURE: NAME/KEY: terminator LOCATION: (73)(100) CTHER INFORMATION: T2 FEATURE:	NAME/KEY: terminator COCATION: (232)(275) COTER INFORMATION: T1 FEATURE:	) NAME/KEY: terminator ; LOCATION: (232)(275) ; OTHER INFORMATION: T1 ; FEATURE:	NAME/KEY: misc_feature ; LOCATION: (332](563) ; OTHER INFORMATION: attP1 recombination site ; FEATURE:	; NAMB/KEY: gene ; LOCATION: (959)(1264) ; OTHER INFORMATION: ccdB gene ; FEATURE:	; NAME/KEY: gene; LOCATION: (1606)(2265); OTHER INFORMATION: Cam(r) gene; FEATURE:	; NAME/KEY: misc_feature ; LOCATION: (2513)(2744) ; OTHER INFORMATION: attp2 recombination site ; PEATURE.	; NAME/KEY: gene ; LOCATION: (2868)(3677) ; OTHER INFORMATION: Kan(r) gene ; FEATURE:	<pre>i NAME/KEY: misc_feature i LOCATION: (3734)(4537) i CTHER INFORMATION: puc oriv / RK2 oriT US-10-357-268-1</pre>	Query Match 24.8%; Score 1108.8; DB 16; Length 4892; Best Local Similarity 99.8%; Pred. No. 2.6e-158; Matches 1110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Wed May 12 08:21:01 2004

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APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: L. XIAO
APPLICANT: L. XIAO
APPLICANT: L. XIAO
APPLICANT: BYED, DEVON R.N.
TITLE OF INVENTUR: OPPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLBIC ACID MC
TITLE OF INVENTUR: US 1042.5120001
CURRENT APPLICANTION NUMBER: US 10/151,690
CURRENT APPLICANTION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICANTON NUMBER: US 60/291,973
PRIOR PRILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
SOFTWARE: PATENTING TOWN S: 64
SOFTWARE: PATENTING TOWN S: 64
SEQ ID NO 62
LENGTH: 4428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4403 ATAGCACACTCTTTTGACATACTTCGGGTA 4372
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US-10-151-690-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 62, Application US/10151690; Publication No. US2003012455A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial
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US-10-151-690-62
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24.8%; Score 1108.8; DB 19
Best Local Similarity 99.8%; Pred. No. 2.7e-158;
Matches 1110; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                  APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: LI, XIAO
APPLICANT: LI, XIAO
APPLICANT: BEDGETTO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REPERENCE: 0942.5120001
CURRENT APPLICATION NUMBER: US,10/151,690
CURRENT FILING DATE: 2002-05-21
PRIOR PILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
SOFTWARE: PARENTEN NUMBER: US 60/291,973
SOFTWARE: PARENTIN NUMBER: US 60/291,973
LINGRAD: LING DATE: 2001-05-21
SOFTWARE: PARENTIN VERSION 3.1
SEQ ID NO 61
LINGTH: 5584
                                      1182 ATAGCACACCTCTTTTTGACATACTTCGGGTA 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: plasmid phonn207
                                                                                                                                                                                                        Sequence 61, Application US/10151690
Publication No. US20030124555A1
GENERAL INFORMATION:
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US-10-151-690-61/c
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Sy da	506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 565 		Query Match 24.6%; Score 1102.4; DB 15; Length 4627; Best Local Similarity 99.5%; Pred. No. 2.4e-157; Matches 1106; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
y da	566 AGGGAGCCTGACATTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 625 	an do	26 GACAAGTITGTACAAAAAAGCTGAACGAGAAACGTAAAAIGATATAAATATCAATATTT 85
Qy Db	626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 685 	<i>ò</i> ₽	86 AAATTAGATTTTGCATAAAAAGAGACTACATAATACTGTAAAACAGAACATACGGTC 145
75 dg	686 TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCACGGGTAAAGTTCACGG 745 	XO QQ	146 ACTATGAATCAACTAGATGGTATTAGTGACCTGTAGTCGACCGAC
čo qa	746 GACATITATCTGACAGCAGACGTGCCAGGGGGATCACCATCCGTCGCCGGGC 805	₩ ₩	206 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCA 265 270 TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACGACAGCCTTCCAAATGTTCTTCTCAA 329
Qy Dp	806 GTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTCT	λ γ	266 ACGGAATCGTGGTATCCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAA 325
Qy Dp	866 GTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCGGTTCAT 925 	96 OX	326 AGAAATAAGAAAAAGAGCGTGCTCTTTTTGTGTGACAAATAAAACATCTACCT 385
op og	926 TTCAATAAACGGGGGGACCTCAGCCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGC 985	ov da	386 ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC 445
op ox	986 ACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACGGAGATATTGACATC 1045	· 영	446 TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 505
Qy Dp	1046 ATATATGCCTTGAGCAACTGATAGCTGTGCGCTGTCAACTGTAATACGCTGCTTC 1105 	& A	506 CTABACGTGATABAGTITCTGTAATTICTACTGTATCGACCTGCGAGCTGGCTGTGTATA 565
δλ	ACCICITITIGACAIACTICGGGTA 1137	λδ 	566 AGGGAGCTGACAITTAIAITCCCCAGAACAICAGGITAAIGGCGITTTTGAIGTCAITT

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626 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACACTGGCCATA 685	දු දු	86 AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAACACACAC
686 TCGGTGGTCATCATGCGCCAGGTTTCATCCCCCGATATGCACCACGGGGTAAAGTTCACGG 745	\$ 64 6	146 ACTATGAATCAACTACTTAGATGGTATTAGTGACCTGTAGTCGACGACAGCCTTCCAAA 205 
746 GAGACITIAICTGACAGCAGACGIGCACIGGCCAGGGGGAICACCAICCGICGCCCGGGC 805	S da	206 IGITCTICGGGIGAIGCIGCCAACITAGTCGACGACGGCCTICCAAAIGIICTICTCAA 265 
806 GIGICAATAAITAICACTCIGTACAITCCACAAACAGACGATAACGGCTCTCTTITTAIAG 865	රු අු	266 ACGGAATGGTGGTATCCAGCCTACTGGTGTTGTCCTCAATGCCGTATTAAATCATAAAA 325 330 ACGGAATGGTGTATCAGCCTACTGGCTATTGTCCTCAATGCCGTATTAAATCATAAAA 389
866 GIGTAAACCTTAAACIGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAAGAGCGGTTCAT 925	දු දු	326 AGAAATAAGAAAAAGAGGTGCGAGCCTCTTTTTTGTGTGACAAAATAAAAACATCTACCT 385 
926 ITCAATAAACCGGGGGACCTCAGCCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGC 985	AQ QQ	386 ATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAAC 445 
986 ACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC 1045	op od	446 TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 505
1046 AIATAIGCCTTGAGCAACTGATAGCIGTCGCTGTCAACTGTCACTGTAATACGCTGCTTC 1105	ò d	506 CTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGACCTGCAGACTGGCTGTGTATA 565
1106 AIAGCACCTCTTTTGACATACTTCGGGTA 1137 	os da	566 AGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 625
	y du	626 TCGCGGTGGCTGAGATCAGCCACTTCTCCCCGATAACGGAGACCGGCACACTGGCCATA 685
Sequence of Application No. US20030124555Al GENERAL INFORMATION:	oy ag	686 TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGATATGCACCGGGTAAAGTTCACGG 745
I. C. T. T. T. T. T. T. T. T. T. T. T. T. T.	oy ap	746 GACACTITATCTGACAGCAGACGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCGGGC 805
TIPE OF INVENTIONS CONTROL OF THE TOTAL OF THE TROUBLE OF THE TROUBLE OF NOCHEL ACLD MOLITIES TO THE TREFERENCE: 0942-5120001 URRENT APPLICATION NUMBER: US/10/151,690 BYRENT FILING DATE: 2022-05-21	Qy Dp	806 GIGTCAATAATAATCACTCTGTACATCCACAAACGGACGGTAACGGCTCTCTTTTTATAG 865 
ALON AFFLIAND NOWBER: US 10/151/690 RIOR FILING DATE: 2002-05-21 RIOR APPLICATION NUMBER: US 60/291,973 RIOR FILING DATE: 2001-05-21	SP GG	866 GIGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAAAGAGCGGTTCAT 925 
NOTIVER OF SEQ ID NOS: 64 SOFTWARE: Patentin version 3.1 EQ ID NO 64 INDIVINE: 4627 TYOP: NAM	ò q	926 TICAAIDAACCGGGGGCGACCTCAGCCATCCTTCTGATTITCCGCTTTCCAGCGTTCGGC 985
ORGANISM: Artificial sequence FEATURE: FORTHRE: FORTHRE: FORTHRE: FORTHRE: FORTHRE: FORTHRE: FORTHRE: FORTHRE: FORTHRE: FORTHRESE FORTHRE: FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRESE FORTHRE	Oy Dp	986 ACGCAGACGACGGCTICATICTGCATGGTIGTGCTTACCAGACCGGAGATATIGACAIC 1045
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o; Agcto	λō	1106 ATAGCACACCTTTTTGACATACTTCGGGTA 1137

Search completed: May 10, 2004, 00:05:14 Job time : 1234.76 secs

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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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US-08-232-016-23
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Sequence 3,
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. /cgn2 / Optodata/2/ina/5A COMB.seq:*
. /cgn2 / Optodata/2/ina/5B COMB.seq:*
. /cgn2 / Optodata/2/ina/6A COMB.seq:*
. /cgn2 / Optodata/2/ina/6A COMB.seq:*
. /cgn2 / Optodata/2/ina/PCTUS COMB.seq:*
. /cgn2 / Optodata/2/ina/PCTUS COMB.seq:*
. /cgn2 / Optodata/2/ina/PCTUS COMB.seq:*
GenCore version 5.1.6
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US-08-064-121-1
US-08-475-975-1
US-09-084-889-1
US-09-084-889-1
US-09-577-424-3
US-09-577-424-3
US-09-577-424-3
US-08-673-768-1
US-08-673-768-1
US-08-673-768-1
US-08-673-768-1
US-08-673-768-1
US-09-225-152A-3
US-09-225-152A-3
US-09-225-152A-1
US-09-225-152A-1
US-09-225-152A-1
US-09-225-152A-1
US-09-225-152A-1
US-09-225-152A-1
US-09-225-152A-1
US-08-961-527-70
US-08-961-527-70
US-08-961-527-70
US-08-961-527-70
US-08-961-527-70
US-08-556-978B-78
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US-07-590-988A-1
US-07-590-988A-1
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Maximum Match 100%
Listing first 45 summaries
                                             - nucleic search, using sw model
                                                                                                                                                                IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Match Length
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Patent No. 592547
GENERAL INFORMATION:
APPLICANT: CORNELSEN, Marc
APPLICANT: SOFTAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: VAN ARSSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                        US-08-814-877-3
US-09-272-432A-3
US-08-229-967-6
US-09-027-169-5
US-09-489-039A-4117
.039A-4117
                                                            US-08-929-967-5
US-08-850-880-3
US-08-944-916-3
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CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-272-432A-3
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US-08-929-967-5
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FILING DATE: 03.NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATE: 30.0CT-1991
FILING DATE: 30.0CT-1991
PRIOR APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30.0CT-1991
APPLICATION NUMBER: GB 92400820.4
FILING DATE: 25.MAX-1992
ATTORNEY AGENT INFORMATION:
NAME: McGowan, Malcolm K
REGISTRATION NUMBER: 939,300
REFERENCE DOCKET NUMBER: 010830-049
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION SEG 10 NO: 23:
SEQUENCE CHRACATESTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
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4052 AAGACTGATTACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGA 4111
                                                                                                                                                                      CATTCAACCCGGTCCAGCACGGCGGCGGGTAACCGACTTGCTGCCCCGAGAATTATGC
                                                                                                                                                                                                                                 CCATTCAACCCGGTCCAGCACGGCGGGCGGGTAACCGACTTGCTGCCCCGAGAATTATGC
                                                                                                                                                                                                                                                                                                                            1298 AGCATTTTTTGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACG
                                                                                                                                                                                                                                                                                                                                                                        4292 AGCATTITITIGGTGTATGTGGGCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                      4358 ACAAATCGTTGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGAC
                                                                                          4112 CACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCCGGTTCCCCGGCGGCGCG
                                                                                                                                         CATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCA
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APPLICANT: SOETAERT, Piet
APPLICANT: STAM, Maike
APPLICANT: STAM, Maike
APPLICANT: BOCKX, Jan
APPLICANT: UNA ARRSEN, Roel
TITLE OF INVENTION: MODIFIED GENES AND THEIR EXPRESSION IN
TITLE OF INVENTION: PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Vigginia
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,016
FILING DATE: 03-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91402920.2
FILING DATE: 30-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92400820.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08232016 Patent No. 5952547 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: F39,300
REFERENCE/DOCKET NUMBER: 0101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: McGowan, Malcolm K
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TYPE: nucleic acid
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COUNTRY: United States
ZIP: 22313-1404
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OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA octopine synthase gene."
FEATURE:
                                                                                                                                                                                                                     LOCATION: 1793..2026
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
OTHER INFORMATION: T-DNA gene 7."
                                                                                               /note= "Coding region of a
truncated modified bt2 (cryIAb) gene, also designated as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (with modified leader with SEQ ID NO. 22."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3812 GITTCGGTTCATTCTAATGAATATATCACCCGTTACTATCGTATTTTTTTATGAATAATA 3871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCGTTCAATTTACTGATTGTACCCTACTACTTATATGTACAATATTAAAATGAAAACA 3937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 5600..6457
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952647
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3698 GTCTAGAGTCCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTT
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                                                                                                                                                                                                                                                                                                                                                         LOCATION: 23967.2921
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 728.8; DB 2;
Pred. No. 3.2e-143;
0; Mismatches 2;
         as pPS0212
         plasmid DNA designated
                                                                                                                                                crylAb6 gene.
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99.7%;
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LOCATION: 7071..7566
OTHER INFORMATION: /fote
OTHER INFORMATION: deriv
OTHER INFORMATION: respe
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NAME/KEY: misc feature
'ACAMTON: 2396..2921
                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 1793..2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: 2922..3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
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Best Local Similarity 99.7
Matches 730; Conservative
                                                                           LOCATION: 1..1785
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
         ORGANISM:
                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-232-016-23
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                                   1136 AAGACTGATTACATAATCTTATTCAAATTTCAAAAGCCCCCAGGGGCTAGTATCTACA
                                                                                                                                                                                                                                                                                                                                                                     4298 AGCATTTTTTGGTGTATGTGGGCCCCCAATGAAGTGCAGGTCAAACCTTGACAGTGACG
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    1058 AAGACTGATTACATAAATCTTATTCAAATTTTCAAAAGGCCCCGGGGGCTAGTATCTACGA
                                                                                           CACACCGAGCGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCCGGCGGGG
                                                                                                                                      4196 CACACCGAGCGGCGACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCCGCCGGCGCG
                                                                                                                                                                                   CATGGGTGAGATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGGAAAGTTACGGGCA
                                                                                                                                                                                                                                                                            CCATTCAACCCGGTCCAGCACGCCGGCCGGGTAACCGACTTGCTGCCCCCGAGAATTATGC
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STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
ZIATE: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08064121
Parent No. 5641664
GENERAL INFORMATION:
APPLICANT: D'IRLUIN, Kathleen
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS FLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE STATEM. E. CONTRELED SOFTWARE STATEM. SOFTWARE PATENTIAN DATA:
APPLICATION NUMBER: US/08/064,121
FILING DATE: 24-MAY-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90403332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-UUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     010830-043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (703) 836-2021
INFORMATION FOR SEO ID NO: 1.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 3006..3665
OTHER INFORMATION: /note= "Coding sequence of
OTHER INFORMATION: chloramphenicol acetyl transferase gene."
FEATURE:
NAME/KEY: misc feature
LOCATION: 3666..4491
OTHER INFORMATION: /note= "3' regulatory sequence
OTHER INFORMATION: containing the polyadenylation site derived from Agrobacteriu
                                                                                                                                                                            /note= "Coding region of a truncated bt2 (cryIAb) gene, also designated bt2 (cryIAb) gene, also designated as the bt884 gen
                                                                                                                                                                                                                                                                                 /note= "3' regulatory sequence
containing the polyadenylation site derived from Agrobacteriu
T-DNA gene 7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3956 CTCCGTTCAATTTACTGATTGTACCCTACTTATATGTACAATATTAAAATGAAAAGA 4015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 5684_.6541
OTHER INFORMATION: /note= "Sequence complementary to
Patent No. 5952547
OTHER INFORMATION: the coding sequence of the beta-lactamase gene."
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NAME/KEY: misc feature
LOCATION: 2480.3005
OTHER INFORMATION: /note= "35S promoter sequence
OTHER INFORMATION: derived from Cauliflower mosaic virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
COCATION: 7155..7639
COTHER INFORMATION: /note= "TR1' and TR2' promoter
COTHER INFORMATION: derived from Agrobacterium T-DNA."
US-08-232-016-22
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Pred. No. 3.2e-143;
0; Mismatches 2;
                                                           ORIGINAL SOURCE:
ORGANISM: plasmid DNA designated as pJD884
                                           DNA (genomic)
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99.7%;
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LOCATION: 18777_2110
OTHER INFORMATION: /note
OTHER INFORMATION: conta
OTHER INFORMATION: T-DNA
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Matches 730; Conservative
                                                                                                                                                       LOCATION: 1..1869
OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS:
                                        MOLECULE TYPE:
                                                                                                                               NAME/KEY:
LOCATION:
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2753 GATTCCTTGAAGTTGAGTATGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAAC 2812
4187 GATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAAC 4246
                                                                                 4247 CCGGTCCAGCACGCCGGCCCGGGTAACCGACTTGCTGCCCCGAGAATTATGCAGCATTTTT
                                                                                                                2813 CCGGTCCAGCACCGCCGGGTAACCGACTTGCTGCCCCCGAGAATTATGCAGCATTTT
                                                                                                                                                                TTGGTGTATGTGGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACGACAAATCGT
                                                                                                                                                                                                       2873 TTGGTGTATGTGGGCCCCCAAATGAAGTGCAGGTCAAACCTTGACAGTGACGACAAATCGT
                                                                                                                                                                                                                                                                                  2933 TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGGGCT 2985
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FILLING DATE: US/08/478,015
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: D'HALLUIN, Kathleen
APPLICANT: GOBEL, BIKE
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES:
ADDRESSEE: BUTIS, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Viginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-1955
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9040332.1
FILING DATE: 23-NOV-1990
RICH APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
PRIOR APPLICATION NUMBER: EP 9140188.2
APPLICATION NUMBER: EP 9140188.2
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TORNEY/AGENT INFORMATION NAME: McGowan, Malocim K. REGISTATION NAMER: 39,300
REGISTATION NUMBER: 91,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08478015
Patent No. 5712135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: plasmid pDE108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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STRANDEDNESS: double
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HYPOTHETICAL: N
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGCGAACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCCGCCGGCGCGCATGGGTGA 4186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2693 GGGGGAACTAATAACGTTCACTGAAGGGAACTCCGGTTCCCCGCCGGCGCGCGTGGGTGA 2752
                                                                                                                                                                                                                                                                                                                                             ATTTACTGATTGTACCCCACTACTATATGTACAATATTAAAATGAAAACAATATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3767 TGTGCACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2333 TGTGCACGTTGTAAAAACCTGAGCATGTGTACCTCAGATCCTTACGCCGGGTTTCGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTCTAATGAATATATCACCGTTACTATCGTATTTTTTATGAATAATATTCTCCGTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTTACTGATTGTACCCTACTACTTATATGTACAATATTAAAATGAAAACAATATATTGT
                                                                                                                                                                                                                                             NAME/KEY: -
LOCATION: 452..1284

LOCATION: 452..1284

OTHER INFORMATION: /label= 3553

OTHER INFORMATION: /note= "3553 promoter sequence derived from OTHER INFORMATION: Cauliflower mosaic virus isolate CabbB-JI"
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                                                                                                                                                                                    /label= pUC18
/note= "pUC18 derived sequence"
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                            ORIGINAL SOURCE:
ORGANISM: plasmid pDE108
                                                                                                                                          NAME/KEY: -
LOCATION: 1..451
OTHER INFORMATION: ,
OTHER INFORMATION: ,
                                                           8
                                     HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-064-121-1
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2873 TIGGIGIATGIAGGCCCCCAAAIGAAGIGCAGGICAAACCIIGACAGIGACGACAAAICGI 2932
                                              4367 TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT 4419
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COCATION: 1..451

OTHER INFORMATION: /note= "pUC18 derived sequence"

OTHER INFORMATION: /note= "pUC18 derived sequence"

OTHER INFORMATION: /label= 3553

OTHER INFORMATION: /label= 3553

OTHER INFORMATION: Cauliflower mosaic virus isolate Cabbb-JI"
                                                                                          2933 reseceserceassecaarrrreceacaacarerceassecreascadescr
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,975
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: D'HALLJIN, Kathleen
APPLICANT: D'HALLJIN, EIKe
TITLE OF INVENTION: PROCESS FOR TRANSFORMIN
TITLE OF INVENTION: MONOCOTYLEDONOUS FLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-UN-1995
CLASSIFICATION: 800
FRIOR APPLICATION: 800
PRIOR APPLICATION DATE: 08/064,121
FILING DATE: 24-MAY-1993
APPLICATION NUMBER: EP 9040332.1
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-UL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REJECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        RESULT 5
US-08-475-975-1
Sequence 1, Application US/08475975
Patent No. 6002070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: plasmid pDE108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 836-2021
FFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 5399 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid_
EDNESS: double
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
LOCATION:
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                                                                                          P
                                                   à
                                                                                                     LOCATION: 452..1284

OTHER INFORMATION: /label= 35S3

OTHER INFORMATION: /note= "35S3 promoter sequence derived from Cauliflower mosai

OTHER INFORMATION: virus isolate CabbB-JI"

FEATURE:
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: -
LOCATION: 2101..3160
OTHER INFORMATION: /label= 3'ccs
OTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
OTHER INFORMATION: site derived from the Agrobacterium T-DNA octopine synthase
OTHER INFORMATION: gene"
                                                                                                                                                                                                                                                    LOCATION: 1285..2100
OTHER INFORMATION: /label= NPTII
OTHER INFORMATION: /note= "coding sequence of neomycine phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGTCCACCACGCGGCCGGGTAACCGACTTGCTGCCCCCGAGAATTATGCAGCATTTTT 2872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGGIGIATIGIGGCCCCCAAATGAAGIGCAGGICAAACCITGACAGIGACGACAAAICGI 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3707 CCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTTCAATTCTGT 3766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2273 CCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTTCAATTCTGT 2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3767 IGTGCACGTTGTAAAAAACCTGAGCATGTGTAGCTCAGATCCTTACCGCCGGTTTCGGTT 3826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3827 CATTCTAATGAATATATCACCCGTTACTATCGTATTTTTATGAATAATATTCTCCGTTCA 3886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2393 CATTCTAATGAATATATCACCGTTACTATCGTATTTTTATGAATAATATTCTCGGTTCA 2452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTATTACAAATCCAATTTTAAAAAAAGCGGCAGAACCGGTCAAAACCTAAAAGACTGAT 4066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2633 TACATAAATCTTATTCAAATTTCAAAAGGCCCCAGGGGCTAGTATCTACGACACACGGG 2692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4187 GATICCTIGAAGTIGAGIAITGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAAC 4246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2753 GATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAAC 2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4247 CCGGTCCAGCACGCGGGCCGGGTAACCGACTTGCTGCCCCGAGAATTATGCAGCATTTTT 4306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2453 ATTTACTGATTGTACCCTACTACTTATATGTACAATATTAAAATGAAAACAATATTATATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3897 ATTTACTGATTGTACCCTACTACTTATATGTACAATATTAAAATGAAAACAATATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.9%; Score 709.8; DB 1; Length 5399; Best Local Similarity 99.7%; Pred. No. 2.7e-139; Matches 711; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
       /label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                                                                                                                  1285..2100
       OTHER INFORMATION: OTHER INFORMATION:
                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                             FEATURE
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APPLICANT: GOBEL, Elke
TITLE OF INVENTION: PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ORGANISM: plasmid pDE108
                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1285..2100
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NAME/KEY:
LOCATION: 1..451
COTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATURE.
NAME/KEY: - 452..1284
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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OTHER INFORMATION: /note= "coding sequence of neomycine
OTHER INFORMATION: /note= "coding sequence of neomycine
FEATURE:
NAME/KEY: -
LOCATION: 2101..3160
OTHER INFORMATION: /label= 3'ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: /polyadenylation site derived from the
OTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4367 TGGGCGGGTCCAGGGCGAATTTTGCGACAACATGTCGAGGCTCAGCAGGACCT 4419
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                                                                                                                                                                                                                                                                                                                                                                        Length 5399;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
LOCATION: 3161..5399
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                   Score 709.8; DB 3;
Pred. No. 2.7e-139;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                      15.9%;
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 711; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                              US-08-475-975-1
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RESULT 6 US-09-084-889-1 ; Sequence 1, Application US/09084889

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OTHER INFORMATION: /label= coding sequence of neomycine OTHER INFORMATION: phosphotransferase gene"

FRATURE:
NAME/KEY: -
LOCATION: 2101..3160
OTHER INFORMATION: /label= 3/ocs
OTHER INFORMATION: /label= 3/ regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from the POTHER INFORMATION: Agrobacterium T-DNA octopine synthase gene"
NAME/KEX: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /label= 35S3
OTHER INFORMATION: /note= "35S3 promoter sequence derived from
OTHER INFORMATION: Cauliflower mosaic virus isolate Cabbb-JI"
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                 ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/084,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36,113
ER: 010830-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 08-JUL-1991
ATTORNSY/AGENT INFORMATION:
NAME: Crane-Felly, Sharon
REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /label= NPTII
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5399 base pairs
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NAME/KEY: -
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LOCATION:
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; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
APPLICANT: Williams, Jan
TITLE OF INVENTION: Maintenance of male-sterile plants
; OORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                         2; Indels
                  OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                            Score 709.8; DB 3;
Pred. No. 2.7e-139;
0; Mismatches 2;
                                                                                                 Query Match
Best Local Similarity 99.7%;
Matches 711; Conservative
3161..5399
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US-08-351-413-2
LOCATION:
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US-09-084-889-1
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LICCATION: complement (397..751)
OTHER INFORMATION: /label= 3'nos
OTHER INFORMATION: /note= "3' regulatory sequence containing the
OTHER INFORMATION: polyadenylation site derived from Agrobacterium
OTHER INFORMATION: T-DNA nopaline synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: complement (1025..1607)
OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /note= "promoter derived from the TA29 gene of OTHER INFORMATION: Nicotiana tabacum"
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OTHER INFORMATION: /note= "3583 promoter sequence derived from
OTHER INFORMATION: cauliflower mosaic virus isolate CabbB-JI"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (752..1024)
WARTION: /label= barster
RMATION: /lote= "coding region of the barstar gene RMATION: Bacillus amyloliquefaciens"
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LOCATION: 2441..3256
CTHER INFORMATION: /label= neo
OTHER INFORMATION: /note= "coding region of the neomycine
OTHER INFORMATION: phosphotransferase gene of In5"
FEATURE:
                                                                                                                            Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= pUC18
/note= "pUC18 derived seguence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: plasmid pVE144 (replicable in E.coli)
                                                                                                                                                                                                                              FILLING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
FILLING DATE: 12-JUN-1992
PRIOR APPLICATION NUMBER: US 07/899,072
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILLING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: SVENSON, LEONARG R:
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10705NATION:
TELEFRAX: (703) 205-8050
ZIP: 2046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
                                                                                                                                                                                 US/08/351,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 6555 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 205-805(
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1608..2440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: complement
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FRATURE:
NAME/KEY:
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NAME/KEY: - 1.396
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complement (397..751)
*RMATION: /label= 3'nos
*RMATION: /note= "3' regulatory sequence containing the
*RMATION: polyadenylation site derived from Agrobacterium
*RMATION: Polyadenylation synthase gene"
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LOCATION: 1608..2440
OTHER INFORMATION: /label= 3553
OTHER INFORMATION: /note= "3553 promoter sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (752..1024)
MANTION: /label= barstex
RMATION: /note= "coding region of the barstar gene
RMATION: Bacillus amyloliquefaciens"
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OTHER INFORMATION: /label= TA29
OTHER INFORMATION: /note= "promoter derived from the OTHER INFORMATION: Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= pUC18
/note= "pUC18 derived sequence"
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE: ORGANISM: plasmid pVE144 (replicable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/899,072
FILING DATE: 12-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/970,849
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: SVEHSSON, Leonard R.
REGISTRATION NUMBER: 30,330
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/351,413
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                               US/09/025,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEK: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6555 base pairs
TYPE: nucleic acid
TYPE: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: complemen
OTHER INFORMATION:
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LOCATION: 1..396
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                  Falls Church
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NUMBER OF SEQUENCES:
                                                                                                                             Virginia
: U.S.A.
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TOPOLOGY: circ
MOLECULE TYPE: I
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FEATURE:
NAME/KEY: -
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NAME/KEY: -
                                                                                                  CITY: Fal
STATE: Vi
COUNTRY:
                                                                                                                                                                                 2046
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                   OTHER INFORMATION: /label= 3.ocs
OTHER INFORMATION: /label= 3.ocs
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyadenylation site derived from Agrobacterium OTHER INFORMATION: T-DNA octopine synthase gene"
NANE/KEY: -
LOCATION: 4316..6555
OTHER INFORMATION: /label= pUC18
OTHER INFORMATION: /note= "pUC18 derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                   3707 CCTGCTTTAATGAGATATGCGAGACGCCTATGATCGCATGATATTTGCTTTCAATTCTGT
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                                                                                                                                                                                                                                                                                                         Score 709.8; DB 1;
Pred. No. 2.9e-139;
0; Mismatches 2;
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US-09-025-583-2
US-09-025-583-2
; Sequence 2, Application US/09025583
; Patent No. 5977433
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.7%;
Matches 711; Conservative
  3257..4315
LOCATION:
                                                                                                                                                                                                                                                          US-08-351-413-2
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         FEATURE:

NAME/KEY:

LOCATION: 241..3256

OTHER INFORMATION: /label= neo

OTHER INFORMATION: /note= "coding region of the neomycine

OTHER INFORMATION: phosphotransferase gene of Tn5"

OTHER INFORMATION: phosphotransferase gene of Tn5"

LOCATION:

LOCATION: 3257..4315

OTHER INFORMATION: /label= 3'ocs

OTHER INFORMATION: /note= "3' regulatory sequence containing the

OTHER INFORMATION: polyademylation site derived from Agrobacterium

OTHER INFORMATION: T-DNA octopine synthase gene"

NAME/KEY:

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                                                                                                                                                                                                                                                                                                                       Length 6555;
                                                                                                                                                                                                                                                                                                                                                  Indels
cauliflower mosaic virus isolate
                                                                                                                                                                                                                                         LOCATION: 4316..6555
COTHER INFORMATION: /label= pucl8
COTHER INFORMATION: /note= "pucl8 derived sequence"
US-09-025-583-583-
                                                                                                                                                                                                                                                                                                                    Score 709.8; DB 2;
Pred. No. 2.9e-139;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.7%;
Matches 711; Conservative
 INFORMATION:
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RESULT 9

US-09-577-424-3

Sequence 3, Application US/09577424

PARENT NO. 6525245

GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR IDENTIFYING COMPONENTS INVOLVED IN SIGNAL
TITLE OF INVENTION: TRANSDUCTION PATHWAYS IN HIGHER PLANTS
FILE REFERENCE: UNL2990

CURRENT APPLICATION NOWBER: US/09/577,424

CURRENT FILING DATE: 2000-05-22

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 3

LENGTH: 14194
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Pred. No. 3.7e-139;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Bacterial Plasmid DNA-Plasmid pZB-ALN
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Best Local Similarity 99.7
Matches 711, Conservative
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12061 ATTCCTTGAAGTTGAGTATTGGCCGTCCGCTCTACCGAAAGTTACGGGCACCATTCAACC 12002
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APPLICANT: Howse, William J.
APPLICANT: Joe, Lawrence K.
APPLICANT: Lee, Kathleen Y.
TITLE OF INTENTION: Delayed Ripening Tomato Plants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,768
FILING DATE: 27-JUN-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 566.4; DB 2;
Pred. No. 3.8e-109;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LL: STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CATE: California COUNTRY: USA
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REFERENCE/DOCKET NUMBER: 012176-005010US
TELECOMMUNICATION INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08673768
Patent No. 5952546
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bedbrook, John R. APPLICANT: Dunsmuir, Pamela
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99.8%;
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nucleic acid
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Best Local Similarity 99.8
Matches 567; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-673-768-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-673-768-1
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                  5428147-1/c
;Patent No. 5428147
; APPLICANT: BARKER, RICHARD F.;KEMP, JOHN D.
; TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
; NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08; Prec. ...
                                                                                                                                                                  APPLICATION NUMBER: US/08/91,538
FILING DATE: 13-UUL-1993
RIOR APPLICATION DATA:
APPLICATION DATA: 86,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1993
APPLICATION NUMBER: 440,432
FILING DATE: 13-NOV-1989
APPLICATION NUMBER: 741,034
FILING DATE: 19-NOV-1983
APPLICATION NUMBER: 144,775
FILING DATE: 20-ANG-1991
APPLICATION NUMBER: 144,775
FILING DATE: 10-NOV-1983
APPLICATION NUMBER: 1624
FILING DATE: 10-NOV-1983
APPLICATION NUMBER: 126,614
FILING DATE: 10-NOV-1983
APPLICATION NUMBER: 20,574
FILING DATE: 10-NOV-1981
APPLICATION NUMBER: 260,574
FILING DATE: 10-NOV-1981
APPLICATION NUMBER: 260,574
FILING DATE: 10-NOV-1981
APPLICATION NUMBER: 848,61
FILING DATE: 10-NOV-1981
APPLICATION NUMBER: 848,61
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FILING DATE: 26-SEP-1983
                                                                                                                                                  CURRENT APPLICATION DATA:
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Matches 707; Conserv
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APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                Score 566.4; DB 2;
Pred. No. 3.8e-109;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13854 ccderccacacacacacacacataacaa 13827
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Patent No. 5910438
                                                                                                                                                                                                     12.7%;
99.8%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                          LENGTH: 15397 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                     Query Match
Best Local Similarity 99.8
Matches 567; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                     STRANDEDNESS: single
                                                                                                             linear
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                                                                                                           TOPOLOGY: li
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7170 IGIGCACGIIGIAAAAAACCIGAGCAIGIGIAGCICAGAICCIIACCGCGGGIIITCGGII 7229
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                                                                                                                                                                                                                          Sequence 1, Application US/08673768
Patent No. 592546
GENERAL INFORMATION
APPLICANT: Bedbrook, John R.
APPLICANT: Bedbrook, John R.
APPLICANT: Howde, William J.
APPLICANT: Lee, Kathleen Y.
APPLICANT: Lee, Kathleen Y.
TITLE OF INVENTION: Delayed Ripening Tomato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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APPLICATION NUMBER: US/08/673,768 FILING DATE: 27-JUN-1996
CLASSIFICATION: 800
RICHA APPLICATION BATA: APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 012176-005010US
TELECOMUNICATION INFORMATION:
TELERPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7677
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-673-768-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08379614
; Befent No. 5910438
; GENERAL INFORMATION:
APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREE: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CAPORT BEACH
STATE: CAPORT BEACH
STATE: CAPORT BEACH
CURRENT APPLICATION NUMBER: US/09/225,152A; CURRENT FILING DATE: 1998-01-04; PRIOR APPLICATION NUMBER: 08/379614; PRIOR FILING DATE: 1995-07-20; NUMBER OF SEQ ID NOS: 10; SCOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2; LENGTH: 420; TYPE: DNA CORDINSM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      858 TITIATAGGIGIAAACCITAAACIGCA 884
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,614
FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/BE93/00051
FILING DATE: 02-AUG-1993
                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KRY: CDS
; LOCATION: (1)...(378)
; OCTHER INFORMATION: ccdB gene of pXIL 18.
US-09-225-152A-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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OPERATING SYSTEM:
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US-08-379-614-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACAC 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 GCCGGGGGTGTCAATAATATCACTCTGTACATCCACAAACAGACGATAACGGCTCTCTC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACAC 677
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Sequence 1, Application US/09225152A
Patent No. 6180407
GENERAL INFORMATION:
APPLICANT: Bernard, Philippe
APPLICANT: Gabant, Philippe
TITLE OF INVENTION: CLONING AND/OR SEQUENCING VECTOR
FILE REFERENCE: VANMA10.001CF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 325.4; DB 2
Pred. No. 3.3e-59;
0; Mismatches 1.
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ccdB gene of pKIL 18
                                                                                                                                                                                                                                                                                                           VANMA10.001APC
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                                                                                                                            PALORASTERCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/BE93/00051
APLING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel B
RESISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMA10.001/
TELEPHONE: 714-760-0404
                                      SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.3%;
Best Local Similarity 99.7%;
Matches 326; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                 OPERATING SYSTEM:
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MOLECULE TYPE: Ge
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US-09-225-152A-2/c
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7.2%; Score 323.2; DB 2; Length 416;
Best Local Similarity 99.1%; Pred. No. 9.5e-59;
Matches 325; Conservative 0; Mismatches 3; Indels 0
                                                                                                                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 base pairs
TERMIDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPEOLOGY: both
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
OXIGINAL SOUNCE:
INDIVIDUAL ISOLATE: ccdB gene of plasmid pXIL 19
FEATURE:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: VANMA10.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEPRAX:
TELEFAX:
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LOCATION: 1...378

OTHER INFORMATION:

US-08-379-614-3
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Search completed: May 9, 2004, 22:13:01 Job time: 195.335 secs

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B (Dases 1 to 698)

L Published Only in DataBase (1998)

E (Dases 1 to 698)

E (Masses 1 to 698)

B (Androi,M., Ibhi,K., Toyoda,A., Shiba,T. and Sakaki,Y.)

Direct Submission

L Submitted (20-AUG-1998) Masahira Hattori, Kitasato University,

Dapartment of Science, JST Sequencing Labbratory; Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail: hattori@hgc.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Fax:0427-78-9561)
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10S0136 T
32283463
P13A3 P1a
P13A3 P1a
P13A5 P1a
EST750020
P11B12 P1
P13B12 P1
P17G11 P1
P27G11 P1
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P27G11 P1
              Homo sapi
OSTR151B2
OSTR151B2
OSTF043E1
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P7-E11 P1
P16A8 Pla
                                                                                   EST754514
P15E7 Pla
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OSTR015E7
OSTR015E7
P20A07 P1
P10-C6 P1
P13-D6 P1
P11-D8 P1
HOMO SAPI
                                                                       Homo sapi
P22B07 Pl
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P20C02 P1
P20H01 P1
P8-E8 P1a
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Homo sapiens genomic DNA, 21q region, clone: f65H12X16, genomic
AG011450
CB997937
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CB1174407
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/wol_type="genomic DNA"
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AG000792
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AG013450
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VERSION
KEYWORDS
SOURCE
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DEFINITION
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AUTHORS
TITLE
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4477
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Maximum Match 100%
Listing first 45 summaries
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CD109790 542 bp mRNA linear EST 15-MAY-2003
AGENCOURT 13988518 NIH MGC 147 Homo sapiens CDNA clone
IMAGE:30346919 5', mRNA sequence.
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(Dases 1 to 542)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 CATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC--ATATGCCTTGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGCTTTCATCCCCGATATGCACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAG
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                                                                                                                                                                                                           11.1%; Score 496.6; DB 29;
ilarity 94.2%; Pred. No. 5.4e-78;
Conservative 0; Mismatches 30;
Tel:0427-78-9732, Fax:0427-78-9561)
Location/Qualifiers
1. 713
Ocganism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="64E11X4"
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1 (bases 1 to 713)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in DataBase (1997)
2 (bases 1 to 713)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (31-077-1997) Masahira Hattori, Kitasato University,
Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             878
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                                                                                                                                                        Gaps
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                                                                                                                                                        4,
                                                                                                                   Length 698;
                                                                                                               Score 518.4; DB 29; Length
Pred. No. 7.5e-82;
0; Mismatches 2; Indels
                                                                                                                                                      0; Mismatches
       /db_xref="taxon:9606"
/chromosome="21"
                                           /map="21q"
/clone="f65H12X16"
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                                                                                                                 11.6%;
98.9%;
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                                                                                                                                                      Matches 553; Conservative
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Department of Science, User Schoolship, Withstato University,

But and a Sakari, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases 1 to 72.3)

E Published Only in DataBase (1997)

L Published Only in DataBase (1997)

E 2 (bases 1 to 72.3)

S Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNA, chromosome 21q

E 2 (bases 1 to 72.3)

S Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.

Direct Submission

L Submitted (31-0CT-1997) Masahira Hattori, Kitasato University,

Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hhttori@hgc.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Fax:042-78-9561)
                                                                 GSS 06-FEB-1999
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                                                                 AG000761 723 bp DNA linear GSS 06-FEI
Homo sapiens genomic DNA, 21g region, clone: 64B11X4, genomic
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Pred. No. 5.6e-63;
0; Mismatches 8;
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/db_xref="taxon:9606"
/chromosome="21"
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Best Local Similarity 98.1%;
Matches 416; Conservative
                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                        survey sequence.
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/clone_lib="NIH MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all_Xho1; Site_2: BamH; Oligo-dT primed using primer
all_Xho1; Site_2: BamH; Oligo-dT primed using primer
size zo 3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NIGRI, National Institutes of Health). Note: This is
a NIH_MGC library."
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                  Tissue Procurement: Dr. Stefan Hansson

CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIRKN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
therp://image.llnl.gov

Plate: NDAM387 row: c column: 24

High quality sequence start: 144

High quality sequence start: 144

High quality sequence Stop: 251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B TonA"
cgapbs-r@mail.nih.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (basa to 522)

1 University (http://mgc.nci.nih.gov/.

1 National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

2 CDA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

2 CDA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/Link at:

http://image.llnl.gov

Plate: NDAM391 row: e column: 05

High quality sequence store: 256.

Location/Qualifiers
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/note="Organ: placenta; Vector: pBluescriptR; Site_1:
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
directionally cloned using primer
5. -TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-lenght clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NGRI,
Mistional Institutes of Health). Note: this is a NIH_MGC
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                                                                                                                                        CB997937 522 bp mRNA linear ES7
AGENCOURT 13894516 NIH MGC_148 Homo sapiens cDNA clone
IMAGE:30348484 5', mRNĀ sequence.
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Pred. No. 1.5e-61;
0; Mismatches 15; Indels
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:30348484"
/tissue_type="pre-eclamptic placenta"
/lab_host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
TTTTGACATACTTCGGGTA 170
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Best Local Similarity 96.2
Matches 435; Conservative
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                          g
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Buxaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Butheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 725)

Homo sapiens genomic DNA, chromosome 21q

Published Only in DataBase (1998)

B 2 (bases 1 to 725)

B Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Direct Submission

U Submitted (07-SEP-1998) Masahira Hattori, Kitasato University,

Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,

Tel:0427-78-9732, Fas.0427-78-5561)

On Feb 5, 1999 this sequence version replaced gi:2951836.

AG005773: Submitted (11-Mar-1998).
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  Homo sapiens genomic DNA, 21q region, clone: f32E9X13, genomic
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llarity 90.2%; Pred. No. 2.3e-62;
Conservative 0; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="f32E9X13"
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AG013450.1 GI:3549208
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Matches 505; Conservat
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OGTRI51B2_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="mixed stage".
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/cone_lba-Ap-wrmcDDA".
/note="The AD-wrmcDDA" library was generated with poly(A) +
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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489 ACGATAACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGT
                                                                                                    TCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCT
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Fax: 617 632 5180

Fax: 617 632 5739

Bemail: Marcy Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans C
cloning project : Contact david_hill@dfci.harvard.edu or

marc_vidal@dfci.harvard.edu
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Contact: Vidal M
Marc Vidal Laboratory
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
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/mol_type="mRNA"
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/sex="Hermaphrodite and male"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Caenorhabditis elegans
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Best Local Similarity 93.6
Matches 383; Conservative
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ACCESSION
VERSION
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CB395230/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           610
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                                                                                                       322
                                                845
                                                                                                                                                                            AACGGCTCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCG 905
                                                                                                                                                                                                                      906 TCAGCAAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCC-TTCCTGATT 964
                                                                                                                                                                                                                                                                                                                                                                          382 reagcaaaagaccerrearrearaaaacggccaccreaccarecrrearra 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    666 TAAGGAGACCGGCACA-TGGCCATAACGGTGGTCATCA-GCGCCAGCTTTCA-CCCCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u> argeaceaeggonraagricaeggaagaerriaaengaeaegaegaegeeegg</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGATCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAG
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                                                                                  TCACCATCCGTCGCCCGGGCGTCTATAATATCACTCTGTACATCCACAAACAGACGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG000763 722 bp DNA linear GSS 06-FEE
Homo sapiens genomic DNA, 21g region, clone: 64EllX4, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TrecgerriceAgegrreggeAcGGAGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 TTTCGCTTTCCAGGTTTCGGCCACGCCAGAC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="64E11X4"
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AG000763.1 GI:2579571
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Best Local 9
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Reboul, J. Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Thierry-Mieg, J., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Brasch, M. A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M. Open-reading frame sequence tags (OSTS) support the existence of at least 17,300 genes in C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACATTTGGAAGGCTGTCGGTCGACTAAGTTGGCAGCATCACCCGAAGAACATTTGGAAGG 3529
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OSTF043E11_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
/clone_lib="AD-wrmcDNA" | /clone_lib="The AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 TTAATACGGCATTGAGGACAATAGCGAGTAGGCTGGATACGACGATTCCGTTTGAGAAGA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 ACATTTGGAAGGCTGTCGGCTAAGTTGGCAGCATCACCCGAAGAACATTTGGAAGG 350
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                         DB 14; Length 487;
                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                      7.8%; Score 347.4; DB 1
96.8%; Pred. No. 1.6e-51;
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Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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B1174407.1 GI:14640210
EST.
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5139
Fax: 617 632 5739
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C. algans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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                                                                                                                                                                                                                        CTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACC 239
                                                                                                   487 TAAAATGATATAAATATCAATATATTAAATTAGATTTTGCATAAAAAAAGACTACATAA 428
                                                                                                                                                                                                                                                                                                                                                       CTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACC
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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/tissue_type="whole animal"
/dev_stage="mixed stage"
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'strain="N2"
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//mol_type="mRNA"
/mol_type="mRNA"
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/db_xref="taxon:6239"
/db_xref="taxon:6239"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into pPC86"
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1 (Dases 1 to 337)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Misaskar,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S. ESTs of Japanese morning glory
Unpublished (2002)
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
Pohliippe_vaglio@dfci.harvard.edu
POLYA=NO.
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                                                                                                                                                                                                                                                      organism="Caenorhabditis elegans'
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BJ555980.1 GI:27237800
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Best Local Similarity 98.2%;
Matches 329; Conservative (
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                                                                                                                                                                                                          FEATURES
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (Dases 1 to 384)
Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T.,
Jackson,C., Shin-i,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.B., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI174407 384 bp mRNA linear EST 09-JUL-2001
OSTF043E11 1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
                                                                                                                                                        /db xref="taxon:6239"
/sex="Hermaphrodite and male"
/sex="Hermaphrodite and male"
/fissue_trpe="whole animal"
/dev stage="mixed stage"
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/clone_lib="AD-wrmcDNA"
/clone="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAAAAACAGACTACATAATACTGTAAAAACACAACATATCCAGTCACTATGAATCAACTA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCCAACTTAGTCGACGGCGTACCAAATGTTCTTCTCAAACGGAATCGTGTAT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAACCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAAAGAAATAAGAAAAG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTAGATGGCTTTAGTGACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGAT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCCTACTCGCTATTGTCCTCAATGCCGTATTAAATCATAAAAAGAAATAAGAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAATACACAGACTACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTIAGATGGTATTAGTGACCTGTAGTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTCATAGTCCTGAAAATCATCTGCATCAAGAACAATTTCACAACTCTTATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 340.2; DB 12;
Pred. No. 3.4e-50;
0; Mismatches 8; ]
                                                                                      /organism="Caenorhabditis elegans"
/mol type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                         cDNAs were cloned into pPC86"
  philippe_vaglio@dfci.harvard.edu
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dana Farber Cancer Institute
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Marc Vidal Laboratory
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FI1F1.5, mRNA sequence.
BI174407
BI174407.1 GI:14640210
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Caenorhabditis elegans
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BI174407/c
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PUBMED
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SOURCE
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247

187

67

EST 18-DEC-2002

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Gaps . 0

+ #5

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/suralimit.../
/sub_species="yoelli"
/db_xref="taxon:7329"
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/note="weetor: pCR4.07D00; lo million Plasmodium yoelli
/note="weetor: pCR4.07D00; lo million Plasmodium yoelli
/note="weetor: pCR4.07D00; lo million plasmodium yoelli
/note="weetor: pCR4.07D00; lo million purified over
infected Anospheles stephensi mosquitoes and purified over
infected Anospheles stephensi mosquitoes and purified over
a pEsc cellulose column. The sporozoites were cultured for
24h at 37c in the presence of $% CO2 and 10% FEB as
described in 'Transformation of sporozoites into early
excerythrocytic malaria parasites dese not require host
cells '( Exp Med. (2003)197(8):1045-50). mRNA was
cells '( Exp Med. (2003)197(8):1045-50). mRNA was
extracted using the Invitrogen microPAST TRACK kit and
used for cDNA construction via the DBBiosciences SMART
cDNA synthesis kit. Double stranded cDNA was cloned into a
plasmid vector using Invitrogen's TOPO TA vector cloning
kit."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 503
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Plasmodium yoelii yoelii
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 1037)
Wang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,
Nussenzweig, V. and Bhanot, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                        organism="Plasmodium yoelii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%; Score 273.2; DB 14; 90.0%; Pred. No. 1.7e-38; tive 0; Mismatches 31;
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location/Qualifiers
                                                                       _type="mRNA"
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Department of Pathology
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Best Local Similarity
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CF469119/c
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Matches
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New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanopol@med.nyu.edu
similar to NR[GI-23483806 hypothetical protein [Plasmodium yoelii
yoelii] (e-108).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGAGGTGCACTGGCCAGGGGGA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 TCACCATCCGTCGCCCGGGCGTGTCAATAATATCACTCTGTACATCCACAAACAGACGAT 322
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                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35883"
/clone="lan08"
/tissue type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"
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Mang, Q., Okubo, E., Kaiser, K., Pashrel, E., Kappe, S., Brown, S.,
Nussenzweig, V. and Bhanot, P.
Expressed sequence tags from Plasmodium yoelii hepatic stages in
axenic culture
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 301.4; DB 12; Length 337; Pred. No. 2.6e-43; 0; Mismatches 1; Indels 1;
                              Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                        1. .337
/organism="Ipomoea nil"
                                                                                                                                                   tshini@genes.nig.ac.jp.
Location/Qualifiers
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                     Tadasu Shin-i
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Local Similarity 99.4%;
nes 313; Conservative
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CF469981/c
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                                                                                                                                                                                                                          /sub species="yoelii"
/db xref="taxon.73239"
/db xref="taxon.73239"
/db sref="taxon.73239"
/lab host="re coli 100H10"
/clone lib="Plasmodium yoelli 17% axenic hepatic stages"
/note="yoector: pCR4.0T0P0; 10 million plasmodium yoelli
/nx sporozoites were isolated from salivary glands of
infected Anospheles stephensi mosquitoes and purified over
a DES2 callulose column. The sporozoites were cultured for
24 at 37C in the presence of 5% CO2 and 10% FBS as
described in 'Transformation of sporozoites into early
                                                                                                                                                                                                                                                                                                                                                                                                                                        excerythrocytic malaria parasites does not require host cells ("O Exp Med. (2003)197(8):1045-50). mRNA was extracted using the Invitrogen microFAST TRACK kit and used for cDNA construction via the BDBiosciences SWART conds synthesis kit. Double stranded cDNA was cloned into a plasmid vector using Invitrogen's TOPO TA vector cloning kit."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 724)
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Homo sapiens genomic DNA, 21g region, clone: 64EllX4, genomic
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New York University School of Medicine
550 First Avenue, MSB 131, New York, NY 10016, USA
Tel: 212 263 5346
Fax: 212 263 8179
Email: bhanop01@med.nyu.edu
No Blast Hits ().
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 271.8; DB 14; Length 91.9%; Pred. No. 3.1e-38; Live 0; Mismatches 24; Indels
                                                                                                                                                                  /organism="Plasmodium yoelii yoelii"
                                                                                                              Blast Hits ().
Location/Qualifiers
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                                                                                                                                                                                          /mol_type="mRNA"
/strain="17X"
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Homo sapiens
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                                                 Published only in DataBase (1997)

2 (bases 1 to 724)

Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.

Burct Submission
Submitted (31-OCT-1997) Masahira Hattori, Kitasato University,
Department of Science, UST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (B-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
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Hattori, M., Ishii, K., Shiba, T. and Sakaki, Y.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1 CVE311874 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS

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LVDQDDLDEEHQGLAPAELFARLKARMPDGEDLVVTHGDACLFNIMVENGRFSGFIDC
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Construct design for efficient, effective and high-throughput gene
silencing in plants
Plant J. 27 (6), 581-590 (2001)
21461301
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                                                                                                                                                                               1157641

2 (bases 1 to 18691)

Materhouse, P.M.

Materhouse, S.D. Submission

Submitted (14-MAY-2001) Waterhouse P.M., Plant Industry,

C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA

Location/Qualifiers
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    .264
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/organism="Flaveria trinervia"
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449. .1442
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/organism="Agrobacterium
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/db_xref="taxon:4227"
17922. .18691
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1443. .7792
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/db_xref="taxon:358"
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/gene="nptII"
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gene="npt11"
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1621 TOGTRACGAMATATTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTT	2461 TTCGCCCCGTTTTCACCATGGGCAATATTATACGCAAGGCGACAAGGTGTTGTCCG 2520 15500 TTCGCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGTTGATGCCG 1559 2521 CTGGCCATTTCACCATGGCCACATGTTTTATACGCAAGGCGACAAGGTGATGCCG 1559 15500 CTGGCCATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAATGCTTAAT 2580 15500 CTGGCCATTCAGGTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAATGCTTAAT 15619 2581 GAATTACAACAGTACTGCCATGAGGTGGCGGGGGGGGGG
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141 CATCARGARCARITTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTG 152 CATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTG 153 CATCAAGAACAATTTCACAACTCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCTGTATCCG 154 CATTTTCACCCTCTATACTTACTAAACGTGATAAAGTTTTCTGTAATTTCTCACTGTATCCG 155 CATTTTCACCCTCTTATACTTACTACAAAATTTCTCTAAAACTTTCTCACAACA	ictgccaacttagtcgactacaggtcactaatacca igaatatgttgtgttttacagtattatgtagtctgt 
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17838 TGAGCAATGCTTTTTTATAATGCCAACTTTGTACAAAAAAGCTGAACGAGAACGTAAAA 17779
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PROTDLLWTYVERLDETTRRALINDLLETSARDESSEILRAVEVTIVVHDDIIENRYP
AKRELQFGEWQRNDILAGIEPBATIDILILLTKAREHSVALVGPARELEDPVPED
DLFPALDETLTLMNSPEPDMAGDERNVYLTLSRIWYSAVTGKTAPKDVAADWAMERLPA
                                                                                                                                                                                                                                                                                                                                     /rranslation="maitlsatslpisariragspaawverlfgydwaqqtiggsdaa
vfrlsaqgrpvlfykydlsgalnelqdeaarlswlattgypcaavldvyteagrdwll
lgevpgqdlsshlapaekysimadamrrhtldpatcpfdhqakhribrargs
                                                                                                                                                                                                                                                                                                                                                                                                LVDQDDLDEEHQGLAPAELFARLKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDC
GRLGVADRYQDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLDEFF"
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                                                                                                                                                                                            /note="neomycin phosphotransferase II (nptII)"
/codon start=1
/transl_table=11
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10706. 11324
/note="right border"
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17922. .18687
/note="octopine esynthase (ocs) terminator"
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/protein id="GA86652.1"
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/db_xref="REMTREMBL:CAC86252"
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|db_xref="taxon:358"
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|db_xref="G1:15982220"
|db_xref="REMTREMBL:CAC86253"
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/function="358 promoter"
/defe. 1628
/gene="pdk"
14660. 16258
                                                                       264. .447
/function="NOS promoter"
448. .1269
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/note="NOS terminator"
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/note="left border"
7793. .9388
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/gene="npt11"
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/gene="spec"
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gene; promoter; speC gene; spectinomycin resistance protein;
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                                                                                                                                        circular SYN 09-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="pHELLSGATE is a derivative of cloning vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
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| organism="Cloning vector phELLSGATE"
| mol type="other DNA"
| db_xref="taxon:167049"
| lab_host="Escherichia coli"
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|mol_type="other DNA"
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/mol_type="other DNA"
/db_xref="taxon:358"
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mol_type="other DNA"
'db_xref="taxon:10641"
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|mol_type="other DNA"
|strain="K12"
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/mol_type="other DNA"
/db_xref="taxon:4227"
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'organism="Escherichia coli"
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Plant J. 27 (6), 581-590 (2001)
21461301
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'db_xref="taxon:358"
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/db_xref="taxon:562"
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Waterhouse, P.M.
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/organism="synthetic construct"
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QY         1021         TTCCGCTTTCCAGCGTTCGGCACGCAGGCGCTTCATTCTGCTTGTCTTAC 1080           Db         1041         TTCCGCTTTCCAGCGTTCGGCACGCAGGCGTTCATTCTGCATGGTTGTGCTTAC 1100           QY         1081         CAGACCGGAGATATTGACATCATATATGCCTTGAGGAACTGATAGCTGTCGCTGTCAACT 1140           Db         1101         CAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACT 1160           QY         1141	### ### ##############################	OY 181 TAAAAACAACATATCAASTCAATTAAATCAATTAGTAATTAGTGACTGTA 240  DD 3735 TAAAACACAACATATCCACTATGAATCAACTTAGATGGTGATTAGTGACCTGTA 3794  OY 241 GTCGACGACGCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGAC

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Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.B.
Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.B.
Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f.Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
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3803. .9019
//organism="Binary vector pJawohl3-RNAi"
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1 (bases 1 to 9019)
Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E. pJawohl8-RNAi a binary vector for gene silencing in plants Unpublished
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|mol_type="genomic DNA"
|fob_xref="taxon:188084"
|fob_cus
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Sols bp DNA circ Binary vector pJawohl8-RNAi, complete sequence. AF408413
AF408413.1 GI:21552736
                                                                                   GAGACCGGCACACTGGCCATATCGGTGGTCATCATGC
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Patent: JP 2002537790-A 180 12-NOV-2002;
INVITROGEN CORP
OR Artificial Sequence
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FN JP-200253790-A/180
FN JP-200253790-A/180
FN JP-NOV-2002
FN O2-MAR-2000 JP 200602252
FR O2-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 FR 28-MAY-1999 US 60/136744
FN JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC C12N15/05,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N15/100
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1 (bases 1 to 5584)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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24.5%; Score 1193; D

Best Local Similarity 100.0%; Pred. No. 4.4

Matches 1193; Conservative 0; Mismatches
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               Indels
Pred. No. 7.8e-168;
; Mismatches 678;
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 llarity 68.8%;
Conservative
 Best Local Similarity
Matches 1777; Conserv
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2940 ACAAGCTAAAGTAACAAATAATATCAAAACTAATAGAAACAGTAATCTAATGTA---

Length 9019;

DB 12;

Score 1152.2;

23.7%;

Query Match

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395 142 130 130 130 130 124 113 113 113 110 110 110 110 110 110 110	SOURCE SOURCE SOURCE Binary vector pJawohl8-RNAi ORGANISM Binary vector pJawohl8-RNAi artificial sequences; vectors.  REFERENCE 1 (bases 1 to 9019) AUTHORS JIREL Diawohl8-RNAi a binary vector for gene silencing in plant JOURNAL AUTHORS 2 (bases 1 to 9019) AUTHORS Direct Submission JOURNAL JOURNAL SIDNIEL BILLE JOURNAL JOURNAL F. Lipka,V., Rademacher,T.R. and Somssich,I.E. AUTHORS JIREL BILLE JOURNAL F. Laberted (08-MUG-2001) Biochemistry, Max-Planck-Institut f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW	ers y vector itc DNA" 188084" ant gene ted seque	/organization branch //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA" //mol type="genomic DNA"
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                                                                                                                                                                                                                                      /translation="mekkitgyttvdisqwhrehfeafqsvaqctynqtvqlditaf
lktvykknktrypafthilatlmnahpeframmkogelvinssvhertytherqotet
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anmonffarapvptmgkxytqgdkylmplalqyhhavcdgffhvgrmlnelqoycdfwqgg
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KVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1762. 2048
/note="contains intron 1 of Arabidopsis thaliana WRKY
/note="contains intron 3"
complement(2073. 3783)
/note="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, CmR gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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/note="attRl of Gateway conversion cassette frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytotoxic protein that is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cassette
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                                                                                       antibiotic
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'note="attR2 of Gateway conversion
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Pred. No. 2.4e-165;
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                                                                                          resistance to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2073. .2199)
/note="attR2 of Gateway
complement (2241. .2546)
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                                                                                                                                                                                            protein_id="AAM62300
db_xref="G1:21552737
                                                                                          function="confers
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gene="CmR"
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intron 27263040   note="RpS5"     note="RpS5"     number=3	Query Match 22.9%; Score 1111.2; DB 12; Length 12677; Best Local Similarity 68.6%; Pred. No. 1.5e-161; Matches 1782; Conservative 0; Mismatches 663; Indels 153; Gaps 12; Qy 1934 CGAGATTTTCAGGAGCTAAAGGAAAGTAAAAAAATCACTGGATATACACCG 1993	4580 CGACATTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAATCACTGGATATACCACGCCGCGTAAATGAGGAAAATCAGTGATATACCACGCCGCGTTTTGAGGCATTTTGAGGCATTTCAGTCAG		OY 2114 ATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCGCCTGATGAATGCTCATC 2173  bb 4400 ATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATC 4341		2234	2294 ACGAITTCCGGCAGTTTCTACACATATTCGCAAAATGTGGCGTGTTACGGGAAAAACC 4220 ACGAITTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACC		OY 2414 TGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTT 2473  DD 4100 TGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACTTCTTCGCCCCCGTTT 4041	OY 2474 TCACCATGGGCAAATATTATACGCAAGGGGACAGGTGCTGATGCCGCTGGCGATTCAGG 2533	OY 2534 ITCATCATGCCGTCTGTGATGCCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGT 2593	2594	Qy 2654 AACAGTATGCGCGCTGATTTTGCGGGGTATAAGAATATATACTGATATGCGG 2713  Db 3860 AACAGTATGCGCGCTGATTTTTGCGCGTATAAGAATATATACTGATATGTATA 3801	Qy 2714 GCCCATAATAGTAATTCTAGCTTTGATGAATTAAATATCAATGATAAAATACTA 2770
Db 3249 ATTCCCCAGAACATCAGGTTATTGATGTCATTTTCGCGGTGGCTGAGATCA 3308  Qy 3880 GCCACTTCTTCCCCGATAACGGCACACTCGCCATTTTCGCGGTGGCTGACTCATCGC 3939  Db 3309 GCCACTTCTTCCCCGATAACGGCACACTCGCCATATCGGTGGTCATCATCGC 3368  Qy 3940 CAGCTTCATCCCCGATAACGGACACCGGCACACTCACGGGAGACTTTATCTGACAGC 3959  Db 3369 CAGCTTCATCCCCCGATATGCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGC 3959  Qy 4000 AGACGTGCACTGCCCGATATGCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGC 3428  Qy 4000 AGACGTGCACTGCCCAGGGGATCACCACCGGGCGTCAATAATAACACTC 4059  A129 AA29 AGACGTGCACTGCCAGGGGATCACCACCGGGCGTCAATAATAACACTC 3488	3489 4120	3549 ATTICACCAGTCCTGTTCTGGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGAC 360 4180 CTCAGCCATCCCTTCCTGATTTCCGCTTTCCAGCGTTCGCACGCA	OY 4240 ATTCTGCATGGTTGTGCTTACCAGACGGAGATATTGACATCATATATGCCTTGAGCAAC 4299	QY 4300 TGATAGCTGTCGCTGTCACTGTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTG 4359	OY 4360 ACATACTTCTGTTCTTGAT 4378  Db 3789 ACATACTTCGGTATACAT 3807	circular	ITION PiggyBac transformation vector pB-UGIR w+, complete SION AY196825 ON AY196825.1 GI:28565731	<b></b>	REFERENCE I Chases I to 120//) AUTHORS Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P. TITLE A toolkit for transformation and mutagenesis in Drosophila using piggyBac	Unpublished 2 (bases 1 to 12677) 3 Griswold, C.M., Roebuck, J., Andersen, F Direct Submission	L Submit Biotec 27709,		repeat_region complement(11>620) /transposon="piggyBac transposable element" TATA_signal 632. 998	

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Hartley, J.L., Brasch, M.A., Temple, G.F. and Cheo, D.
Compositions and methods for use in recombinational cloning
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CO 12N15/09,CONT4/00,CI2N1/15,CI2N1/21,CI2N5/10,CI2N15/PC

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CO 12N15/09,CI2N1/15,CI2N1/21,CI2N5/10,CI2N15/PC

CO 12N15/09,CONT4/00,CI2N1/15,CI2N1/21,CI2N15/PC

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CO 12N15/09,CONT4/00,CI2N1/11/20,CI2N1/21,CI2N1/21,CI2N15/PC

CO 12N15/09,CONT4/00,CI2N1/11/20,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/21,CI2N1/2
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                                                                                                                                                                                                                                                      TCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATCATATATGCCTTGAGCA 4297
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#P 2002537790-A 157 12-NOV-2002;

#P 2002537790-A 157 12-NOV-2002;
                                                                                              GCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAAACGGGCG
                                                  4118 GCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCG
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    .4208
    /organism="synthetic compostable type="genomic DNA" /db_xref="taxon:32630"

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PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DAVID CHEO PC C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC 00, C12N5/00 CC pDONR204 CC n is any nucleotide CO nis any nucleotide Location/Qualifiers FF Key Location (1326). (1326).
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0; Mismatches 8;
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Best Local Similarity 98.8%;
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Haldimann, A. and Wanner, B.L.
Direct Submission
Submitted (29-UUL-2001) Biological Sciences, Purdue University,
Lilly Hall, West Lafayette, IN 47907, USA
Location/Qualifiers
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                                  Length 4782;
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                                    DB 12;
                                  Score 876.4; DB 12;
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Best Local Similarity 71.6%;
Matches 1259; Conservative
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                 GCATTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCC
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EPDTRPQVHGNI.SPLAEATRKLDPTRP.ITCVNVMFCDAHTDTI.SDL.FDVLCLNRYYGW
YVQSGDLETAEKVLEKELLAWQEKLHQP.I.ITEYGVDTLAGLHSMYTDMWSEEYQCAM
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                                                         Sciences, Purdue University,
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.larity 71.6%; Pred. No. 2.3e-125;
Conservative 0; Mismatches 441;
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Submitted (29-JUL-2001) Biological Science
Lilly Hall, West Lafayette, IN 47907, USA
Location/Qualifiers
                                                                                                                                                                      1. 6742
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/mol_type="genomic DNA"
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Haldimann, A. and Wanner, B.L.
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/transl_table=11
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NL Patent: JF 2002537790-A 156 12-NOV-2002;

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OS Artificial Sequence
PN JP 2002537790-A/156

PD 12-NOV-2002

PF 02-WAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR

O2-MAR-1999 US 60/136744

PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC

C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/10, C12N15/ PC

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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(656)..(961)
(1099)..(1184)
(1303)..(1962)
(2210)..(2442)
(2565)..(3374)
      3358 AGAATATATACTGATATGTATACCCGA 3384
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Best Local Similarity 98.5%;
Matches 854; Conservative
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                                                                                                                                                                                                        ecceecteargaargercarcesaarrecerarescaarsaaagacestgagerg 1714
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                                                                                                                                                                                                                                                                                                                                                                                                                           TCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT 2331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2392 TICGICICAGCCAAICCCIGGGIGAGITICACCAGITITIGALTIAAACGIGGCCAAIAIG 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2452 GACAACTICTICGCCCCCCGTTITCACCATGGGCAAATATTATACGCAAGGCGACAAGGTG 2511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1473 GACAACTICTICGCCCCCGTITICACCAIGGGCAAATATTATACGCAAGGCGACAAGTG 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1653 TCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT
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                                             TITITAAAGACCGTAAAGAAAAATAAGCACACAAGTITITATCCGGCCTITATTCACATICIT
                                                                                                                                       GCCCGCCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGACGGTGAGCTGGTG
TITITAAAGACCGTAAAGAAAATAAGCACAAGTITITAICCGGCCTTTAITCACATICIT
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Job time : 12150.6 secs
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	Description	Abg82130 Acceptor	Abg82141 Acceptor			Abg82130 Acceptor	Aac55521 Donor pla	Abz58767 Destinati	Ada50329 Plasmid v	Aac55525 Donor pla	Aac55632 Donor pla	Abz58766 Donor pla	Abz58768 Destinati	Abz58769 Destinati	Abz58770 Destinati	Aac55524 Donor pla	Aac55523 Donor pla	Donor	Abz58768 Destinati	Aac55521 Donor pla	Abz58767 Destinati	Abz58769 Destinati	Abz58770 Destinati	Adas0329 Plasmid v
SUMMARIES	ΩI	ABQ82130	ABQ82141	ABQ82143	ABQ82142	ABQ82130	AAC55521	AB258767	ADA50329	AAC55525	AAC55632	ABZ58766	ABZ58768	ABZ58769	ABZ58770	AAC55524	AAC55523	AAC55522	AB258768	AAC55521	ABZ58767	ABZ58769	ABZ58770	ADA50329
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	% Query Match	100.0	52.7	52.0	51.6	30.1	24.5	24.5	24.5	24.5	24.5	24.5	24.4	24.4	24.4	22.0	21.2	17.4	17.4	17.4	17.4	17.4	17.4	17.4
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## ALIGNMENTS

Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds. Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13. (CSIR ) COMMONWEALTH SCI & IND RES ORG. Helliwell C; ABQ82130 standard; DNA; 18691 BP. 26-JAN-2001; 2001US-0264067P. 29-NOV-2001; 2001US-0333743P. 24-JAN-2002; 2002WO-AU000073. (first entry) Wesley S, Waterhouse P, WPI; 2002-682669/73 WO200259294-A1 11-DEC-2002 01-AUG-2002. Synthetic. RESULT 1 ABQ82130 

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA.

Claim 13; Page 62-72; 104pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bacherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites, (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and

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fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present invention
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Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;

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	18691; 0;	SCAACA         CAACA	AGAAAC        AGAAAC	FACATA         FACATA	PAGTGA        FAGTGA	STCGAC STCGAC	CTATTO		SAAAA         SAAAA		CTACTO	PACATO	FCCCC FCCCC		CTGGC
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`	т,	CCTGT        CCTGT	AAGCT	AAAAA       AAAAA	TAGAT       TAGAT	TGCCA 	AGCCT.	GTGCG	TCATA        TCATA	ACAAG	TCTGT       TCTGT	TATTC       TATTC	AGCCA       AGCCA	CCAGC	CAGAC
1	DB 6	AGTGA       AGTGA	CAAAA	GCATA        GCATA	CTACT	GATGC	TATCC	AAGAG        AAGAG	TAGTG	CTCTT	AAGTT	ATTTA        ATTTA	AGATO	ATGCG	GACAG
	Score 4861; Pred. No. 0; Mismatches	ACTGAT	TTTGTP	SATTTI         SATTTI	AATCAP	rcggg1 	rcgrcg 	aagaaa         aagaaa	ATACGC        ATACGC	ACTTTTA 	STGATA        STGATA	CTGAC	TGGCTC 	STCATC        STCATC	FTATCI
ì	core red. Nisma	TTTTG        TTTTG	CCAAC	AATTAC	CTATG	STICT	CGGAA.	GAPAT	TTCAT	CTTAT	TAAAC       TAAAC	GGGAG(        GGGAG(	CGCGG	CGGTG 	AGACT
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	ACAAACAGA	ACAAACAGA	CAGTCCCTGTTCT	CATCCCTTCCTGATT	CATGGTTGTGCTTAC	GTTGTG	GCTGT	FICGCTGTCA	GGGTAGTGC            GGGTAGTGC	PACAGGGACA	AACAGGGACA	AAGT	GCAAAGT	CTAAGTAGTTGA'	AGTT	5-1	TATG	GCTTTCTTGTAC		ggtcactat          ggtcactat	GGTACCC	GGTACCC	GTTAAGTGATGT	STGATG	AAAT	ATAAATA	3TAAGACGAA	STAAGACGAA	AAGAT	cargraagarg	GATCACTACCGGGC
	CACTCTGTACATCC	-	CTTAAACTGCATTTCAC	GGGCGACCTCAGCC	ATTCTG	ATTCTG	aactgatag	AACTGATAG	CITITIGACAIACIT 	CCGGTAT	CCGGTAT	CAGGTATTTATT	-F	CTAATACCAT	CTAATACCAT	TAGTCTGT	ragrerer	40TTG0TTC		TTGCAACGAACA(               TTGCAACGAACA(	TCCTCGAGGAATTC	TCCTC	AAAAT	ATAAAATA	TGAAAAATAA	TGAAAAATAA	GACA	GACAAGTGA	AATTTGATCGA	AATTTGATCGA	taatgaaataagat
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	CACCATCCGT	ACCATCCGT	AACGGCTCTCTC	TCAGCAAAAGAGCCGTTC                 TCAGCAAAGAGCCGTTC	CCGCTTTCCAG	CCGCTTTC	AGACCGGAGATA	ACCGGAGAT		ACGTCTCA	GTCTC	SGATTATTTATT	SATTATTTATT	CGGGTGATGCTG	grander	TAGTGACTGG	TAGTGACTGG	TAATTTAATATATT 		TTGGCATTATAAGAA              TTGGCATTATAAGAA	- 25 −	CAAAATAAAATCAT	GGAAAT	TAAGG?	TAGTATGATTATAN'	GTATG	TAAA	TACATAAAC	Fi —	raaaagrig	tacgcccgtaa 
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1920   NTACGGCCGGGTAGAGGTTTTCACAGAGCTAAATGAAATG

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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia on 01; (D) selectable marker region capable of being expressed in the recipient cell; region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites, (iii) first, second, third and polymeration region functional in the eukaryotic cell. The first and courth recombination sites, or the second and third recombination sites are identical. The first and second recombination site, and preferably are identical. The first and second recombination site, and preferably are identical. The first and second recombination site, and preferably are identical. The first and second recombination site, or the third and same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic are also as a second sequence. The vectors can also be used to convert a DNA fragment in the second sequence of double-stranded RNA which can be used to convert a DNA fragment in the second sequence of the convert and present and second sequence of the convert and second second second and sequence of the convert and second second second second convert and second second second second convert and second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of doublestranded RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAACTTTGTACAAAAAGCTGAACGAGAAACGTAAAATGATATAAATTTCAATATATTT
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Matches 3651; Conservative
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TAACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTC
                                      17120 TAACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTC
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1522 IGCTTATCAATTGTTGCAACGAACAGGTCACTATCAGTCAAATAAAT	14193 ILLIIILCCIIIINGIBARARATINIINGISIIIITTACATAATAAATATATATATAAATAAATAAAAAAAA	14613 AAIGTAAAAAATGGACAAGTGATGTGTAAGACGAAGAAAAAAAGTTGAGAGTAAGT 1821 ATAITTTAAATGAATTTGATCGAACATGAAGATGAATGAATAAAGCGCGGTAAGGGTTC 1821 ATAITTTTAATGAATTTGATCGAACATGTAAGATGAATAATACGGCGGGTAAGAGGTTC 181 ATAITTTTAATGATTGATCGAACATGTAAGATGAATAATACGGCGGTAAGAGGTTC 1821 ATAITTTTAATGATTGATCGAACATGAAGATGATGATGATAAAAAAAA	14673 ATATTATTTTTAATGAATTTGATCGAACATGAAGATGATAATTTTTTGAGTTATCGAGATT 1940 1881 CAACTTTCACCATAATGAAATAAGATCACTACCGGGCGTATTTTTTGAGTTATCGAGATT 1940 14726	1941 ITCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAATCACTGGATATACCACCGTTGATAT 14726	1	14726	14726	14726	14726	14726	14726	14726	y 2481 GGGCAAATATTATACGCAACGACGAGGGGGCTGATGCGCTGGCGGTTCAGGTTCATCA 2540 b 14726	2541 TGCCGTCTGTGATGCCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGA	b 14726 14726 14726 14726 y 2601 TGAGTGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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TGCATCAAGAACAATTTCA TGCATCAAGAACAATTTCA TGGATTTTCAGCCTCTATA TGGATTTTCAGCCTCTATA TGGATTTTCAGCCTCTATA	13505 CTAAACGIGATAAAGITTCTGTAATTCTACTGTATCGACCTGCAGACTGGCTGTATA 13564 622 AGGCAGCCTGACATTATATATCCCCAGAACATCAGGTTAATGGCGTTTTGATGTCATTT 681 13565 AGGCAGCTGACATTATATATCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTT 681	682 ICGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 741 [11		3745	DARIAATATCACTCTGTACATCCACAAACAGACGATAACGCTCTCTTTTTTAGAACACTTAAAACGCATTACACTTTCACGTCAACAAAAGAGCGCGTTCATAAACCTTAAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCGCGTTCATAAACTTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCGCGTTCAT	982 ITCAATAAACCGGGGGACCTCAGCCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTCGGC 1041 13925 ITCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATTTTCCGCTTTCCAGCGTTGGCC 13984	1042 ACGCAGACGACGGCTTCATTCTGCATGGTTGTGCTTACCAGACCGGAGATATTGACATC 1101 13985 ACGCAGACGACGGGCTTCATTCTGCATGGTTGTGCTTACCAGACGGAGATATTGACATC 14044	1102 ATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACTGTCATGTAATACGCTGCTTC 1161	1162 ATAGCACCTCTTTTGACATACTTCGGGTAGTGCCGATCAACGTCTCATTTTCGCCAA 1221 	1222 AAGTTGGCCCAGGGCTTCCCGGTATCAACAGGACACCAGGATTTATTT	82	1342 GTCGACTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGGATATGTTGT 1401	02 GTTTACAGTATATGTAGTATTTTTTTTTTTTTTTTTTTT	45 GITTITACAGITATITATATATATATATATATATATATATATATATAT	A ATAICALTITACGITICTCGITICTGTTCTTGTACAAAGTGG

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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bacherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter or egion capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and courth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and courth recombination sites, or the second and third recombination sites, are identical. The first and second recombination site, and preferably are identical. The first and second recombination site, or the third and same recombination sites, do not recombination site, or the third and same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic and sequences. The vectors can also be used to convert a DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene for reduction of the phenotypic expression of nucleic ne present sequence represents an acceptor vector nucleotide
                                                                                                                                                                                                   Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.
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                                                                                                                                                                 Acceptor vector pHELLSGATE 12 nucleotide sequence SEQ ID NO:26.
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                                              TGTTCTTCGGGTGATGCTGCCAACTTAGTCGACCGACAGCCTTCCAAATGTTCTTCTCAA
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14165 AAGTTGGCCCAGGGCTTCCCGGTATCAACAGGGACACCAGGATTTATTATTCTGC 1282 TGATCTTCCGTCACAGGTATTTATTCGGCGCAAAGTGCGTCGGGGTGATGCTGCCAA [		1402 GTTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTTGTATT 	1462 ATATCATTITAGGITICICGTICAGCITICITGTACAAAGITGGCAITAIAAGAAAGCAI		1582 CATCCAGCTGCAGGAATTCGGTACCCA-ATTGGTAAGGAAATTAATT	14448					1941 TICAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAAATCACTGGATATACCACCGTTG	14726	14726	14726		zibi uugaraangaraangaragarangarahangaanangangilatikan 14726	2241 GETTITCCAIGAGCAAACIGAAACGIITTICAIGGCICTGGAGIGAAIACCAGGAGITI	14726	2301 CCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTA
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3329 TTGATAAGCAATGCTTTCTTATAATGCCAACTTTGTACAAAAGCTGAACGAGAAAAGCT 3388	463 TACCTGCACAAGCTTGGATCCTCTAGACCACTTTGTACAAGAAAGCTGAACGAGAAACGT 1552 389 AAAATGATATAAATATCAATATTAAATTAGATTTTGCATAAAAAACAGACTACATAAT 3448	523 AAAATGATATAAATATCAATATATTAAATTAGATTTTGCATAAAAAACAGACTACATAAT 1558 449 ACTGTAAAACACAACATATCCAGTGACTATGAATCAACTACTTAGATGGTATTAGTGAC 3508 	15583 ACTGTAAACACAACATATCCAGTCACTATGAACTCACTTAGATGGTATTAGTGACC 15642 3509 TGTACTCGACTAAGTTGGCAGCATCACCGACCACTTTGCGCCGAATAAATA	69 0	3629 GGGCCAACTTTTGGCGAAAATGAGGGTTGATCGGCACTACCCATTTCACAACTCTTATA 3688	3689 CITITUTCITACAAGTCGITCGGCTTCATCTGGATTTTCAGCCTCTATACTAACG 3748 15815 CITITCTCTTACAAGTCGTTCGGCTTCAGATTTTCAGCCTCTATACTAAAGG 15874	3749 IGAIDAAGITICTGTAATITCTACTGTATCGACCTGCAGACTGGCTGTATDAAGGGAGC 3808	3809 CTGACATTATATTCCCCAGAACATCAGGTTAATGGCGTTTTTGATGTCATTTTCGCGGT 3868	3869 GGCTGAGATCAGCCACTTCTTCCCGATAACGGAGACCGGCACACTGGCCATATCGGTGG 3928	3929 TCATCATGCCCAGCTTCATCCCCCCATAGCACCACCGGGTAAAGTTCACGGGAGACTT	3989 TATCTGACAGACGTGCACTGCCAGGGGGATCACCATCCGTCGCCCGGGCGTGTCAA	TAATATCACTCTGTACATCCACAAACAGAGGATAACGGCTCTCTTTTTATAGGTGTAAA 	4109 CCTTAAACIGCATTICACCAGICCCTGTICTCGTCAGCAAAGAGCCGTTCATTICAATA 4168	9 AACCGGGGCGACCTCCGTGCTTCCGCGATTTCCGGCTTTCGGGGTTCGGCAGA	とり てり	s carcecerrearrers	4289 CCTTGAGCAACTGATGCTGTCACTGTCAACTGTCATAATACGCTGCTTCATAGCAC 4348 	4349 ACCTCTTITGACATACTTCTGTTCTTGATGCAGGATGATTTTCAGGACTATGACACTAGC 4408	9 GTATATGAATAGGTAGATGTTTTTTTTTTTGTCACACAAAAAGAGGCTCGCACCTCTTTT 4468
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replication allowing operably linked replication allowing replication in a rata such as Escherichia coli; (b) being expressed in the recipient cell comprising: (i) promoter or promoter by RNA polymerases of a enkaryotic se, (ii) first, second, third and transcription terminating and
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                                                                                                                                                                                                                                                                    TACAGTATTATGTAGTCTGTTTTTTATGCAA 4708
GGCTGTCGGTCGACTAAGTTGGCAGCATCAC 4588
                                                                                                                                                                                                                                                                                                                                         CATTITACGITICCGITCAGCITITITGIA 4768
                                                                               ATTGAGGACAATAGCGAGTAGGCTGGATACG 4528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA fragments having an origin of
chimeric DNA construct, useful for
producing large amounts of double-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nbinational cloning; silencing;
NA; plant; ds.
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GAGACTITATCTGACAGAGAGAGGTGCACTGGCCAGGGGGGATCACCATCCGTCGCCCGGGC 13804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTAGATTTTGCATAAAAAACGACTACATAATACTGTAAAACACAACATATCCAGTC 13144
polyademylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombination sites, or the third and same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silending target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breading scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic accordance from the present sequence represents an acceptor vector nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAATTAGATTTTGCATAAAAAACAGACTACATAATACTGTAAAAACACAAAATATCCAGTC
                                                                                                                                                                                                                                                                                                                                         DB 6; Length 17458;
                                                                                                                                                                                                                                                                                                 Sequence 17458 BP; 4487 A; 4367 C; 4332 G; 4272 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                     Score 2510.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                              from the present invention
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Matches 3628; Conservative
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	15		TCGAACATGAATAACAAGGTAACATGATAGATCATGTCATTGTGTTATCATTGATCATGA		15220 CATTIGGATIACATIACTIACCTTAAGCTIGGATCCTCTAG 15265				15267			3442 ACATAATACTGTAAAACACAACATATCCAGTCACTATGAATCAACTACTTAGATGGTATT 3501		3502 AGTGACCTGTAGTCGACTAGCTTGGCAGCATCACCCGACGCACTTTGCGCCGAATAAATA	15413 AGTGACTGTAGTTGACTAAGTTGGCAGCATCACCCGACGCACTTTGCGCCGAATAAATA	3562 CCTGTGACGGAAGATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGG 3621	15473 CCTGTGACGGAAGATCACTTCGCAGAATAAATAAATCCTGGTGTCCCTGTTGATACCGGG 15532		15533 AAGCCTGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGGATTTCACAAC 15584		15585 TCTTATACTTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 15644	3742 CIAAACGIGAIAAAGITICIGIAATITICIACIGIAICGACCIGCAGACIGGCIGIGIAIA 3801		3802 AGGGAGCCIGACATITATATICCCCAGAACATCAGGITAATGGCGTTTTTGATGTTTT 3861	Н	2 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACGGCACACTGGCCATA 3	5 TCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 1	3922 TCGGTGGTCATCATCATGCCCCAGCTTTCATCCCCCATATGCACCACCGGTAAGTTCACGG 3981	825 TUGGTGGTGGTLATLATGGGCLAGGTTTCATCCCCGATAGGCACCGGGGTAAAGTTAAGGCAAAAAAAA	15885 GAGACTITAICTGACAGGACGTGCACGGCCAGGGGGATCACCATCGTCGCCCGGGC 15944	4042 GIGICAAIAAIAICACICIGIACAICCACAAACAGACGAIAACGGCTCTCTTTTAIAG 4101	15945	4102 GIGIAAACCITAAACHGCAITICACCAGICCCTGITCTCGICAGCAAAAGAGCCGITCAI 4161 
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16605 TATGCAAAATCTAATTTAATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTT 16664
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Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds. Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13. (CSIR ) COMMONWEALTH SCI & IND RES ORG Helliwell C; ABQ82130 standard; DNA; 18691 BP 24-JAN-2002; 2002WO-AU000073 2001US-0264067P. 2001US-0333743P. entry) Waterhouse P, (first WO200259294-A1. 26-JAN-2001; 29-NOV-2001; 01-AUG-2002 11-DEC-2002 Wesley S, Synthetic. ABQ82130, 

2002-682669/73

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-RNA

62-72; 104pp; English Claim 13; Page The present invention describes a vector (I) comprising operably linked CC DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coll; (b) selectable marker region capable of being expressed in the recipient cell cr and (c) a chimeric DNA construct comprising: (i) promoter or promoter cregion capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and control recombination sites; (iii) 3' transcription terminating and courth recombination region functional in the eukaryotic cell. The first and capable of reacting with a same recombination sites, or the second and third recombination sites are identical. The first and second recombination sites, or the third and contrib recombination sites, do not recombination sites, or the third and contributed RNA which can be used for silencing large amounts of double-stranded RNA which can be used for silencing large muchaic control or into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic conserved for acids requence represents an acceptor vector nucleotide sequence from the present invention

Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 U; 0 Other;

9 Query Match
30.1%; Score 1462.6; DB 6; Length 18691;
Best Local Similarity 59.4%; Pred. No. 4.2e-194;
Matches 2920; Conservative 0; Mismatches 1889; Indels 104;

17838 TGAĞCAATGCTTTTTTATAATGCCAACTTTGTACAAAAAGCTGAACGAAAACGTAAAA 17779 120 61 TGAGCAATGCTTTTTTATAATGCCAACTTTGTACAAAAAAGCTGAAACGAAAAAAA CGGGCCCCAAATAATGATTTTTTTTTTGACTGATAGTGACCTGTTCGTTGCAAATTTGA

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CATCAAGAACAGAACTATGTCAAAAGGGTGTGCTATGAAGCAGCGTATTACAGTG 17362  GATTTTCAGCCTCTATACTTACTAAACGTGATAAAGTTCTGTAATTTCTACTGTATGGA 600	GAGACCGGCACACTGGCCATATCGGTGGTCATCATGGCCAGGTTTCATCCCCGATATGC 780  CTGACGAGAACAGGGACTGGTGAAATGCAGTTTAAGGTTTACACCTATAAAGA 17131  ACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGGACGGTGACAGGGGG 840  ACCACCGGGTAACGTTTGTGGATGTACAGAGTGTATTATGACACGCCGGGGG 840  GAGAGCGTTATCGTTTGTGGATGTACAGAGTGATATTATGACACGCCGGGGG 17071  ATCACCATCGTCGCTCGTCAATAATATCACTGTCAGAACTCTCCCGTGAACTT 17011  TAACGGCTCTTTTATAGGTGAACCTTAAACTGCATTCACCAGTCCCT 954  TAACGGCTCTCTTTTATAGGTGAAAACTGGCATTCACCAGTCCCT 954  TAACCGGTGGTGCATATCAGGGAAAAACTGGCATTCACCACAATAGGCCAGT 16951	GITCTCGTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGGGCCTCCGGCAATCCTTC 1014	4 3 0 5 6 6 5 4 4 8 9 3 0 6 6 5 6 6 5 6 6 5 6 6 5 6 6 6 6 6 6 6
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Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.5%; Score 1193; DB 3; 100.0%; Pred. No. 1e-156; iive 0; Mismatches 0;
                                                                        Donor plasmid pDONR201 nucleotide sequence.
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                 AAC55521 standard; DNA; 4470
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Best Local Similarity
Matches 1193; Conserva
                                                                                                                              Bacteriophage lambda
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28-MAY-1999;
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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, and attB2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity comprising one or more mutated att recombination sites of molecule (III) comprising one or more mutated att recombination sites of molecule comprising at recombination between a first nucleic acid molecule comprising a second recombination site and a second nucleic acid molecule att recombination site. (1), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production of polypeptides and antibodies. The present sequence is in the exemplification of the present invention
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                                                                                                             CCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCA
                                                                                                                                                                            361 ATGCCGTATTAAATCATAAAAGAAATAAGAAAAAAGAGGTGCGAGCCTCTTTTTGTGTG
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0; Mismatches 0;
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24.5%;
Best Local Similarity 100.0%;
Matches 1193; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecules encoding an attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful recombinational cloning of polypeptides.
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24.5%; Score 1193; DB 3;
Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 1193; Conservative 0; Mismatches 0;
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28-MAY-1999;
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5144 ACAAATAAAAACATCTACTATTCATATACGCTAGTGTCATAGTCCTGAAAATCATCTG
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concoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2

concolotide sequence. Also described are: (1) an isolated mucleic acid

molecule (II) comprising one or more att recombination sites comprising

concomprising one or more region that increases the specificity

comprising one or more mutated att recombination sites and a second att

comprising one or more mutated att recombination sites comprising at

comprising one or more mutated att recombination sites comprising at

comprising one or more mutated att recombination sites comprising at

comprising at second recombination site and a second mucleic acid molecule

comprising a second recombination site that interacts with the mutated

comprising a second recombination site that interacts with the mutated

comprising a second recombination site that interacts with the mutated

comprising a second recombination site that interacts with the mutated

comprising a second recombination site that interacts with the mutated

control mucleic acid molecules. They can be used for changing vectors, targeting

concleic acid molecules. They can be used for changing vectors, targeting

desired proteins, operably linking nucleic acid molecules of interest to

congress to intracellular locations, cloning into phages and

cloning (I), (II), (II), host colls and vectors can be used in the

production of polypeptides and antibodies. The present sequence is used

in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
recombinational cloning of polypeptides.
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99US-0126049P.
99US-0136744P.
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Matches 1193; Conserv
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                                                                      GATTITICAGCCTCTATACTTACTAAACGTGATAAAGTTTCTGTAATTTCTACTGTATCGA
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Best Local Similarity 100.0%; Pred. No. 1e-156;
Matches 1193; Conservative 0; Mismatches 0; Indels 0;
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represents the destination plasmid pDONR212 nucleotide sequence
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                                                                                         Inserting a population of nucleic acids into a second target selecting and isolating nucleic acid molecules by mixing the population of nucleic acid with a second target nucleic acid.
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llarity 99.7%; Pred. No. 7.9e-156;
Conservative 0; Mismatches 4;
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1140 1020 1997 1937 Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid. 1577 1637 1697 raacggcrichtritataggreiaaaccritaaacrecarricaccagrecergricic 1817 1877 Arcaccarcerceceeeeeefercaraarararecrereracarcaaacaeeea 1757 960 840 900 720 780 CAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTGGCTGTCACT Grchechalagaecegrrcarricalhalaceeceacercaecearecrreerr CAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACT ATGGCGTTTTTGATGTCATTTTCGCGGTGGCTGAGATCAGCCACTTCTTCCCCGATAACG :s18 Aréscéritridarercarriricécésiéscréadarcascéririricécésaraacs 1578 GAGACCGCACACTGGCCATATCGGTGGTCATCATGCGCCCAGCTTTCATCCCCGGATATGC ACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGG ATCACCATCCGTCGCCCGGGCGTGTCAATATATCACTCTGTACATCCACAAACAGACGA TAACGGCTCTCTTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTC GTCAGCAAAAGAGCCGTTCATTTCAATAAACCGGGCGACCTCAGCCATCCCTTCCTGATT TTCCGCTTTCCAGCGTTCGGCACGCACACGGCGCTTCATTCTGCATGGTTGTGCTTAC TICCGCTTTCCAGCGTTCGGCACGCAGACGACGGGCTTCTTCTTCTGCATGGTTGTGCTTAC GAGACCGGCACACACGCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCCCGATATGC 1193 GTCACTGTAATACGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTA recombination; nucleic acid selection; ds. Destination plasmid pDONR212(F) nucleotide sequence. DRN; Byrd Esposito D, BP. 21-MAY-2002; 2002WO-US015947. 21-MAY-2001; 2001US-0291973P. ABZ58769 standard; DNA; 4627 Li X, (first entry)

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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid phonNE212(F) nucleocide sequence
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Query Matches Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches Of Grant Matches O	Local Similarity 99.7%; Score 1186.6; DB 7; Length 4627; Local Similarity 99.7%; Pred. No. 7.95-156, Sept. 10. 6aps 0;  1 coccoccanariantratarization and sept. 10. 7.95-156, Sept. 10. 7.95-156, Sept. 10. 7.95-156, Sept. 10. 7.95-156, Sept. 10. 7.95-156, Sept. 10. 7.95-156, Sept. 10. 7.95-156, Sept. 10. 7.95-156, Sept. 10. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8. 8.
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represents the destination plasmid pDONR212(R) nucleotide sequence sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other; sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 U; 0 Other; set Local Similarity 99.7%; Pred; No. 7.9e-156; A; Indels 0; Gaps 0; atches 1189; Conservative 0; Mismatches 4; Indels 0; Gaps 0; occeptions of 1 CGGGCCCCAAATAATGATTTTATATTTGACTGATAGTGACCTGTTGCTTGC	121 TGATATAAATATCAATATTAAATTAGATTTTGCATAAAAACGACTACATAATACTG 180  129 TGATATAAATATCAATATTAAATTAGATTTTGCATAAAAAACAGACTACATAATACTG 180  181 TAAAACACAACATATCAATATTAAATTAGATTTTGCATAAAAAACAGATTACTGACTG	01 CCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATTCCAGCCTACTCGCTATTGTCCTCA 36   CCTTCCAAATGTTCTTCTCTCAAACGGAATCGTCGTATTCCAGCCTACTCGCTATTGTCCTCA 36   CCTTCCAAATGTTCTTCTTCTCAAAGGAAAAAGGAAAAAGGGTGCGGCTACTCGCTATTTGTCCTCA 36   ATGCCGTATTAAATCATAAAAGAAATAAGAAAAAAGAGGTGCGGAGCCTCTTTTTTGTGTG 42   ATGCCGTATTAAAATCATAAAAGAAATAAGAAAAAAGAGGTGCGAGCCTCTTTTTTTGTGTG 42   ATGCCGTATTAAAATCATAAAAAAAAAAAAAAAAAAAAA	CATCAAGAACAATTTCACAACTCTTATACTTTCTCTTACAAGTCGTTCGGCTTCATCTG 54( CATCAAGAACAATTTCACAACTCTTATACTTTTCTTTACAAGTCGTTCGGCTTCATCTG 54( CATCAAGAACAATTTCACAACTCTTATACTTTTCTTTACAAGTCGTTCGGCTTCATCTG 54( GATTTTCAGCCTCTATACTTACTAAAGGTTACTGTAATTTCTGTAATTTCTACTGTATCGA 60( CATCACACACCTCTATACTTACAAAGATTACTGTAATTTCTCTATCTGTATCGA 60( CATCACACACTCGTTATAAAGGGAGCCTGACATTATATTTCCCCAGAACATCAGGTTA 66( CTGCAGACTGGCTGTATAAAGGGAGCCTGACATTATATTTCCCCAGAACATCAGGTTA 66( CTGCAGACTGGCTGTATAAAGGGAGCCTGACATTTATATTCCCCAGAACATCAGGTTA 66( CTGCAGACTGGCTGTATAAAGGGAGCCTGACATTATATTCCCCAGAACATCAGGTTA 66( CTGCAGACTGTATATCAGGAGCCTGACATTATATTCCCCCAGAACATCAGGTTA 66( CTGCAGACTGTATATCAGGAGCCTGACAATAACGGTTA 66( CTGCAGAACTGTATAAAGGGAGCCTGAAAACGTTAAAACGATAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAACGATAAAACAAAC	CGCGGTGGCTGAGATCAGCCACTTCTTCCCCGAIAAU CGGTGGTCATCATGCGCCAGCTTTCATCCCCGGTATG CGGTGGTCATCATGCGCCAGCTTTCATCCCCGGTATG CGGTGGTCATCATGCGCCAGCTTTCATCCCCGGTATG AGACTTTATCTGACAGCAGAGCTGCACTGGCCAGGGG AGACTTATCTGACAGAGAGCGTGCACTGGCCAGGGG TGTCAATAATATCAGCTGTACATCCACAAACAGAG TGTCAATAATATCACTTGTACATCCACAAACAGAG TGTTAAACCTTAAACTGCATTTCACCAGTCCTTTCTTTTTTCATGTTTTTTTT

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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1 and attB2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising at comprising a second recombination site that interacts with the mutated att recombination site. (I) (III) primers, vectors and methods att recombination site. (I) (III) primers, vectors and methods from the present invention are used for the recombinational cloning of mucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins,
                                                                                                                                                                                                                                                            CAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACT 1140
                                                                                                                                                                                                                                                                                                                                 CAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACT 1148
969 GICAGCAAAAGAGCGGITCAIITITTAAIAAACGGGGGCCTCAGCCAICCCTICCTGAIT 1028
                                                                                                                                                                        1029 TICCGCTTICCAGCGTICGGCACGCAGACGACGGCTICATTCTGCATGGTIGTGCTTAC 1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 teriophage lambda; att; recombination site; attB; attB; attL; attL; attL; attL; ecombinational cloning; entry vector; destination vector; le product targeting; fusion tag cleavage; ds.
                                                                                                                  Trecectificaacatreacaacaacaacaacaacaacatreatreacaracatrate
                                                                                                                                                                                                                                                                                                                                                                                                             1141 GTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTGACATACTTCGGGTA 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1149 GTCACTGTAATACGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTA 1201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheo D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or plasmid pDONR204 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Temple GF,
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changing copy number, changing replicons, cloning into phages and cloning. (1), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention
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                                                                             22.0%; Score 1068.2; DB 3; larity 98.8%; Pred. No. 2e-139; Conservative 0; Mismatches 8;
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Matches 1088; Conserv
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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APPLICANT: Reznikoff, William S
APPLICANT: Reznikoff, William S
APPLICANT: Chart. Igor Y
APPLICANT: Zhou, Hong
TITLE OF INFORTION: System for in vitro Transposition
NUMBER OF SEQUENCES: 11
CORRESPENDENCE ADDRESS: 2
ADDRESSE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,880
US-09-481-355-24

US-09-481-355-24

US-09-485-659A-24

US-09-484-996-24

US-09-479-123-24

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US-09-115-475-13

US-09-115-475-13

US-09-358-856C-2

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NAME/REY: CDS
NAME/ARY: 77..1267
OTHER INFORMATION: /function= "tetracycline"
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Flasmid DN
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CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BETSON, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9602
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEFRAX: 608-251-9166
                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/08850880
; Patent No. 5925545
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NAME/KEY:
LOCATION:
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NAME/KEY:
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JS-08-944-916-3/c
                                                                                                                                                                                                         STATE: WI COUNTRY:
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                                                                                                                                                                                                                                Length 5838;
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                                                                                                                                                                 LOCATION: 4715..5530
CTHER INFORMATION: /function= "kanamycin resistance"
US-08-850-880-3
                                                                                                                                                                                                                               15.6%; Score 759.2; DB 2;
ilarity 99.0%; Pred. No. 1.2e-141;
Conservative 0; Mismatches 8;
                                                 LOCATION: complement (2301..2960)
OTHER INFORMATION: /function= "chloramphenicol
OTHER INFORMATION: resistance"
             resistance'
                                                                                                                    insertion seq 4564..4582
            OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                      Similarity
                                                                                                                  NAME/KEY:
LOCATION:
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Best Local Simi
Matches 764;
                                              NAME/KEY:
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Length 5838;
Sequence 3, Application US/08944916
Sequence 3, Application US/08944916
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goryshin, Igor Y
APPLICANT: Zhou, Hona L
APPLICANT: Zhou, Hona L
APPLICANT: Zhou, Hons L
APPLICANT: Zhou, Hons, System for In Vitro Transposition
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
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OTHER INFORMATION: /function= "kanamycin resistance"
US-08-944-916-3
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No. 1.2e-141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,916 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function= "tetracycline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 08/814,877
APPLICATION NUMBER: US 08/814,877
FILING DATE: 09-SEP-1996
PRIOR APPLICATION DATA: US APPLICATION NUMBER: US PILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Plasmid DNA"
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LOCATION: complement (2301..296
OTHER INFORMATION: /function= "
OTHER INFORMATION: resistance"
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REFERENCE/DOCKET NUMBER: 9602:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEPHONE: 608/251-5000
TELEPHONE: 608/251-5000
TELEPHONE: 608/251-5000
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99.0%;
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4564..4582
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LOCATION: 1..19
FEATURE:
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MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,877
FILING DATE:
CLASSIFICATION: 435
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OTHER INFORMATION: /function= "chloramphenicol
OTHER INFORMATION: resistance"
FEATURE:
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99.0%; Pred. No. 1.2e-141;
tive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 77..1267
OTHER INFORMATION: /function= "tetracycline
OTHER INFORMATION: resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              960296.94142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Plasmid DNA"
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 9602
TELEPHONE: 608/251-5000
TELEPHONE: 608/251-5000
TELEPHONE: 608/251-5000
INFORWATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 5338 base pairs
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4564..4582
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LOCATION: 1..19
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Best Local Similarity 99.09
Matches 764; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                           Conservative
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US-08-814-877-3/c
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                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: complement (2301..2960)
OTHER INFORMATION: /function= "chloramphenicol resistance"
                                                                                                                                                                          /function= "tetracycline resistance"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
; LOCATION: 4715..5530
CTHER INFORMATION: /function= "kanamycin resistance"
US-09-272-432A-3
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                                                                                                                                                                                                                                                                                                                                                           insertion seq
4564..4582
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Best Local Similarity 99.0
Matches 764; Conservative
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4715..5530
                                                                                                                 NAME/KEY: CDS
LOCATION: 77..1267
OTHER INFORMATION:
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APPLICANT: Reznikoff, William S
APPLICANT: Govybhin, Igor Y
APPLICANT: Govybhin, Igor Y
APPLICANT: Lou, Hong
TITLE OF INVENTION: System for In Vitro Transposition
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: I South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 53703
COMPUTER: BLORPY disk
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,432A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.96277
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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DESCRIPTION: /desc = "Plasmid DNA"
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Patent No. 6437109
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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STREET: 1 C.
TTY: Madison
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CLONE: DRZTL1
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US-09-272-432A-3/c
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Sequence 23, Application US/09479122

Sequence 23, Application US/09479122

Patent No. 6410266

GENERAL INFORMATION:
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERF. BRUCE

APPLICANT: SHERF. BRUCE

APPLICANT: SHERF. BRUCE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

TITLE OF INVENTION: ENDOGENOUS GENES

TITLE OF INVENTION: ENDOGENOUS GENES

TITLE OF INVENTION: ENDOGENOUS GENES

TITLE OF INVENTION: ENDOGENOUS GENES

CURRENT APPLICATION NUMBER: US/09/479,122

CURRENT FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: 09/159,643

PRIOR FILING DATE: 1997-09-26

PRIOR FILING DATE: 1997-09-26

PRIOR FILING DATE: 1997-09-26

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

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                     TOGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT
                                                                         2674 TCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGAT
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SEQ ID NO 23
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NAME/KEY: modified base

'OCTION: (8499)

'OCTION: (8499)
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Matches 764; Conserv
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APPLICANT: RIERF, BRUCE
APPLICANT: RIERF, BRUCE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
CURRENT APPLICATION NUMBER: US/09/479,122
CURRENT APPLICATION NUMBER: 09/276,820
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-02-19
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOSTWARE: PACENTIN VEY: 2.1
SEDGTH: 9737
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15.6%; Score 759.2; DB 4;
Best Local Similarity 99.0%; Pred. No. 1.4e-141;
Matches 764; Conservative 0; Mismatches 8;
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                                                                                                                                                     Sequence 22, Application US/09479122
Patent No. 6410266
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APPLICANT: HARRINGTON, JOHN J.
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COTHER INFORMATION: a, c, US-09-479-122-22
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ORGANISM: Homo sapiens
                                                                                                    RESULT 5
US-09-479-122-22/c
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Pred. No. 1.4e-141;
0; Mismatches 8;
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US-09-484-997-22/c
; Seguence 22, Application US/09484997
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Best Local Similarity 99.0%;
Matches 764; Conservative (
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                                                                                                                                                                                       OTHER INFORMATION: a, c, t,
SEQ ID NO 28
TENGTH: PLENGTH: PARAMETER DIAM
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: modified base
LOCATION: (8347)
OTHER INFORMATION: a, c, t
NAME/KEY: modified base
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US-09-479-122-28
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Fatent No. 641026

GENERAL INFORMATION;

APPLICANT: HARRINGTON, JOHN J.

APPLICANT: HARRINGTON, JOHN J.

APPLICANT: BIBER;

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF TITLE OF INVENTION: ENDOGENOUS GENES

FILE REFERENCE: 0221-0003C

CURRENT APPLICATION NUMBER: US/09/479,122

CURRENT APPLICATION NUMBER: 09/276,820

FRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VET. 2.1
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APPLICANT: HARKLEGION, CORN O.
APPLICANT: HARKLEGION, CORN O.
APPLICANT: HARKLEGION, CORN O.
APPLICANT: RUNDLETT STEPHEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGRADUS GENES
FILE REFERENCE: 0221-0003J
CURRENT PELLING DATE: 2000-01-18
PRIOR FILING DATE: 1999-03-26
PRIOR PAPLICATION NUMBER: 09/276,820
PRIOR PAPLICATION NUMBER: 09/276,83
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-02-19
PRIOR PELING DATE: 1999-02-19
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GENERAL INFORMATION:
APPLICANT: HARRINGTON, JOHN J.
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OTHER INFORMATION: a, c, t, NAME, KEY: modified base
LOCATION: (8499)
OTHER INFORMATION: a, c, t,
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                                                APPLICANT: HARRINGTON, JOHN J.

APPLICANT: HARRINGTON, JOHN J.

APPLICANT: SHERF, BRUCE

APPLICANT: SHERF, BRUCE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

TITLE OF INVENTION: ENDOGENOUS GENES

FILE REPERENCE: 0221-0003J

CURRENT APPLICATION NUMBER: US/09/484,997

CURRENT APPLICATION NUMBER: US/09/766,820

PRIOR APPLICATION NUMBER: 09/376,820

PRIOR FILING DATE: 1999-03-26

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PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

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PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 33

SOFTWARE PARCHIN VINCE: 2.1

SEQ ID NO 22
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Pred. No. 1.4e-141;
0; Mismatches 8;
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Best Local Similarity 99.0%;
Matches 764; Conservative (
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, OTHER INFORMATION: a, c, t,
US-09-484-997-22
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OTHER INFORMATION: a, c,
NAME/KEY: modified_base
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                       GENERAL INFORMATION:
APPLICANT: HARRINGTON,
APPLICANT: SHERF, BRUC
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Patent No. 6524824
GENERAL INFORMATION:
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERF. BRUCE
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF TITLE OF INVENTION: ENDOGENOUS GENES
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                                                                                                                   Query Match 15.6%; Score 759.2; DB 4; Best Local Similarity 99.0%; Pred. No. 1.4e-141; Matches 764; Conservative 0; Mismatches 8;
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CTHER INFORMATION: a, c, t, NAME/KEY: modified base LOCATION: (8499)
OTHER INFORMATION: a, c, t,
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US-09-481-355-22/c
                                                               ; OTHER INFORM
US-09-484-997-28
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APPLICANT: HARRINGTON, JOHN J.
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHEEF, BRUCE
APPLICANT: SHEEF, BRUCE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGENOUS GENES
FILE REFERENCE: 0221-0003J
CURRENT PEPLICATION NUMBER: 03/276,820
PRIOR PRILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-09-26
PRIOR FILING DATE: 1999-09-26
PRIOR FILING DATE: 1999-09-26
PRIOR FILING DATE: 1999-09-26
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATECHTIN VONER: 09/253,022
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATECHTIN VONER: 09/253,022
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATECHTIN VONER: 09/253,022
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATECHTIN VONER: 09/253,022
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATECHTIN VONER: 09/253,022
PRIOR FILING DATE: 1999-02-19
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                                                                                  TITITAAAGACCGTAAAAAAAAAAAAAAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTT
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Patent No. 6524818
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FEATURE:
NAME/KEY: modified base
LOCATION: (8347)
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US-09-484-997-28/C
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Sequence 23, Application US/09481355
Fatent No. 6524824
GENERAL INFORMATION,
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERF, BRUCE
APPLICANT: RINDLETT, STEPHEN
TITLE OF INVENTION: CONFOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION: ENDOGENOUS GENES
TITLE OF INVENTION UNDER: 0521-0037F
CURRENT PILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-03-24
FRIOR PRIOR APPLICATION NUMBER: 09/159, 643
FRIOR FILING DATE: 1999-09-24
FRIOR APPLICATION NUMBER: 09/159, 643
FRIOR FILING DATE: 1999-03-08
FRIOR FILING DATE: 1999-03-08
FRIOR FILING DATE: 1999-03-08
FRIOR FILING DATE: 1999-03-08
FRIOR FILING DATE: 1999-03-08
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FRIOR FILING DATE: 1999-02-19
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Pred. No. 1.4e-141;
); Mismatches 8;
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; OTHER INFORMATION: a, c,
US-09-481-355-23
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OTHER INFORMATION: a, c,
NAME/KEY: modified_base
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-481-355-23/c
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Pred. No. 1.4e-141;
0; Mismatches 8;
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                              US/09/481,355
FILE REFERENCE: 0221-0003F
CURRENT PAPLICATION NUMBER: US/09/481,3
CURRENT FILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 09/159,643
PRIOR PELING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1999-03-66
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR PRIOR PRIOR NUMBER: 09/263,814
PRIOR FILING DATE: 1999-03-08
PRIOR PRIOR PRIOR NUMBER: 09/253,022
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SEQ ID NO 2:
LENGTH:: 9737
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Best Local Similarity 99.0%;
Matches 764; Conservative
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OTHER INFORMATION: a, c, t,
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OTHER INFORMATION: a, c,
NAME/KEY: modified_base
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APPLICANT: HARRINGTON, JOHN J.
APPLICANT: BRIGE
APPLICANT: SHERF, BRUCE
APPLICANT: RUNDLETT, STEPHEN
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: EMDGEMOUS GENES
FILE REPERENCE: 0221-0038F
CURRENT FILING DATE: 2000-01-12
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PRIOR FILING DAIE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR PELING DATE: 1999-03-24
PRIOR PELING DATE: 1998-09-24
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-66
PRIOR PELING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/253,022
PRIOR APPLICATION NUMBER: 09/253,022
PRIOR PILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
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Patent No. 6524824
GENERAL INFORMATION:
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CTHER INFORMATION: a, C,
US-09-481-355-28
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OTHER INFORMATION: a, c,
NAME/KEY: modified_base
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ORGANISM: Homo sapiens
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US-09-481-355-28/c
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LENGTH: 9737
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Pred. No. 1.4e-141;
0; Mismatches 8;
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PACENT NO. 6541221
GENERAL INFORMATION:
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERF BRUCE
APPLICANT: SHERF BRUCE
APPLICANT: SHERF BRUCE
APPLICANT: NUNDIETT, STEPHEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: ENDGENOUS GENES
TITLE OF INVENTION: ENDGENOUS GENES
TITLE REPERENCE: 0221-0003US
CURRENT PILICATION NUMBER: US/09/481,282
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PRIOR APPLICATION NUMBER: 09/159,643
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 08/941,223
PRIOR FILING DATE: 1997-09-26
 al Similarity 99.0%;
764; Conservative
 Best Local Similarity
Matches 764; Conserv
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US-09-481-282-22/c
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                                                                                     US-09-401-282-23/C

US-09-401-282-23/C

Sequence 23, Application US/09481282

Patent No. 6541221

GENERAL INFORMATION:

APPLICANT: HARRINGTON, JOHN J.

APPLICANT: SHERF, BRUCE

APPLICANT: SHERF, BRUCE

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: COMPOSITIONS GENES

FILE REFERENCE: 0221-0003US

CURRENT APPLICATION NUMBER: 09/09-643

PRIOR APPLICATION NUMBER: 09/159, 643

PRIOR FILING DATE: 1999-09-24

PRIOR FILING DATE: 1999-09-26

PRIOR FILING DATE: 1999-09-26

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VENTER: 09/253,022

PRIOR FILING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VENTER: 09/253,022

PRIOR FILING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 33

LENGTH: 9737
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ORGANISM: Homo sapiens
ORGANISM: Boadified base
LOCATION: (8347)
OTHER INFORMATION: a, c, t
FEATURE:
NAME/KEY: modified_base
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Best Local Similarity 99.0°
Matches 764; Conservative
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Pred. No. 1.4e-141;
0; Mismatches B;
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  PRIOR APPLICATION NUMBER: 09/263,814
PRIOR FILING DATE: 1999-03-08
PRIOR PRING DATE: 1999-02-19
PRIOR PILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATEURIN Ver. 2.1
SEQ ID NO 22
LENGTH: 9737
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764; Conservative
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NAME/KEY: modified_base
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Matches 764; Conserv
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2272 TC	2614 GT	2392 TT	2554 TT	2452 G	2494 G	2512 C	2434 C	2572 A	2374 AS	
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Search completed: May 9, 2004, 22:12:56 Job time: 214.917 secs 64, Appl 1, Appli 61, Appl 63, Appl 20, Appl 23, Appl 37, Appl

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Sequence 13, Application US/10055001A

Publication No. US20030049835A1

Publication No. US20030049835A1

Publication No. US20030049835A1

APPLICANT: Waterhouse, Per APPLICANT: Waterhouse, Per APPLICANT: Waterhouse, Per APPLICANT: Helliwell/Christopher A.

TITLE OF INVENTION: using recombinational cloning

TITLE OF INVENTION: using recombinational cloning

FILE REFERENCE: HELLGA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT APPLICATION NUMBER: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

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NAMB/KEY: misc_feature
LOCATION: (17850)..(17659)
OTHER INFORMATION: attP1 recombination site (complement)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (10706)..(11324)
CHER INFORMATION: right T-DNA border fragment
FEATURE:
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LOCATION: (11674)..(13019)
OTHER INFORMATION: CAMV35S promoter fragment
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LOCATION: (7922)..(9985)
OTHER INFORMATION: spectinomycin resistance
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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         NAME/KEY: misc feature
LOCATION: (17610)..(16855)
OTHER INFORMATION: ccdB selection marker (complement)
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| LOCATION: (2149)..(2706)
| OTHER INFORMATION: a left T-DNA border region
US-10-055-001A-13
                                                                                                                                                                                     site
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NAME/KEY: misc_feature
LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1443)...(2148)
OTHER INFORMATION: nopaline synthase gene
FEATURE:
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NAME/KEX: misc_feature
LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombination
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NAME/KRY: misc_feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine synthase
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LOCATION: (13048)..(13279)
OTHER INFORMATION: attPl re
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Matches 4861; Conservative
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NAME/KEY: misc feature
LOCATION: (497)...(1442)
OTHER INFORMATION: nptII
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LOCATION: (1443)..(214)
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OY 4681 AGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATGTTATTATATCAT 4740  Db 17720 AGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATTATATATA	US-10-055-001A-23  Sequence 23, Application US/10055001A  Publication No. US2003004983SA1  Publication No. US2003004983SA1  Publication No. US2003004983SA1  Publication No. US2003004983SA1  APPLICANT: Waterhouse, Peter  APPLICANT: Waterhouse, Peter  APPLICANT: Hallwell, Christopher A.  TITLE OF INVENTION: Wethod and means for producing efficient silencing con;  TITLE OF INVENTION: Using recombinational cloning  FILE REPERBNCE: HELLGA  CURRENT APPLICATION NUMBER: US/10/055,001A  CURRENT APPLICATION NUMBER: US/10/055,001A  CURRENT FILING DATE: 2002-06-11  SEQ ID NO 23  LANGTH: 17862  LANGTH: 17862  LANGTH: 17862  CURRENT SPRINES  CONSANISM: Actificial sequence  FRIUMER  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURES  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT  PERFURENT	Duery Match  64.9%; Score 3154.4; DB 15; Length 17862;  Best Local Similarity 82.6%; Pred. No. 0;  Matches 4015; Conservative 0; Mismatches 16; Indels 831; Gaps  1 CGGGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTTCGTTGCAAAATTGA  13040 CGGGCCCCAAATAATGATTTTTTATTTTTGATAGTGAACCTGTTCGTTGCAAAAATTGA  131040 CGGGCCCCAAATAATGATTTTTTTTTTTTTTTTTTTTTT	Db 13160 TGATATAAATATCAATATAAATTTGCATAAAAACAGACTACATAATACTG 13219  Db 13160 TGATATAAATATCAATATAAATTAGCATAAAAACAGACTACATAATACTG 13219  Oy 181 TAAAACACAACATATCCAGTCACTATGAATCACTTAGATGGTATTAGTCACTCTTA 13279  Db 13220 TAAAACACAACATATCCAGTCACTATGAATCACTTAGATGGTATTAGTCACCTGTA 13279  Oy 241 GTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCCACCTGTA 13279  Db 13280 GTCGACCGACAGCCTTCCAAATGTTCTTCGGGTGATGCTGCCAACTTAGTCCACCGACAG 13339  Oy 301 CCTTCCAAATGTTCTTCTCAAACGGATCGTCGTACTTAGTCGACCGAC
16580 GCACTTTGCGCCGAATAAATACCTGTGACGGAAGATCACTTCGCAGAATAAATA	16880 ATGGCGTTTTTGGCGGTGGCTGAGATCAGCCACTTCTTCCCGATAACG  3901 GAGACCGCCACACTGGCCATATCGGCGGGGCTGAGATCAGCCACTTCTTCCCCGATAACG  16940 GAGACCGGCACACTGGCCATATCGGCGGCTGATCAGCCACACTTCTTCCCCGATATGC  3961 ACCACCGGCACACTGGCCATATCGGTGGTCATCATCAGCCACACTTCATCCCGATATGC  3961 ACCACCGGCACACTGGCCATATCGGTGGTCATCAGCAGCTTTCATCCCGATATGC  3961 ACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACACAGCTTTCATCCCGATATGC  4021 ATCACCATCCGTCGGCGGGAGACTTTATCTGACACAGCAGCGGGGGGGG	17180 GTCAGCAAAGAGCCGTTCATTTCAATAACCGGGGACCTCAGCCATCCTTCCT	4381 AGATGATTTTCAGGACTATGACACTAGCGTAT 17420 AGATGATTTTCAGGACTATGACACTAGCGTAT 4441 ACACAAAAAAGAGGCTCGCACCTCTTTTTCTT 17480 ACACAAAAAAGAGGCTCGCACCTCTTTTTCTT 4501 GAGGACAATAGCGAGTAGCTGGATACGACACACACACACA

961 GTCAGCHAMGGGCGTCAMTCCAMTCCAMTCCAMTCCAMTCCAMTCCA
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15390   GARTITICAGCCTCTATACTAACCTGATAAAGTTCCGGAATCTCTGTATCCCTATACCTGTATACCTGTATAACCTCTCTATACCTGATAAACCTCTCTCT
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13565 AGGAGCCTGACATTATATTCCCCAGAACATCAAGGTTATTGATGTCATT 1362.  682 TCGCGGTGGCTGACATTTATATTCCCCGATAACGGAGACCGGCACATTTGATGTCATT 1362.  13625 TCGCGGTGGCTGACACTCTTCTCCCCGATAACGGAGACCGGCACACTGGCCATA 741  13625 TCGCGGTGGCTGAGACCACTTCTTCCCCGATAACGGAGACCGGCACACTGGCCATA 1368.  742 TCGCTGGTCATGCGCCACGCTTTCATCCCCGATAACGAGAGACCGGGTAAAGTTCACGG 801	13685 TCGGTGGTCATCATGCGCCAGCTTTCATCCCCGGATATGCACCGGGTAAAGTTCCCCC  802 GAGACTTTATCTGACAGCGTGCACTGGCCAGGGGGATCACCATCCGTCGCCCC  13745 GAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGATCACCATCCGTCGCCCCC  862 GTGTCAATAATATCACTCTGTACATCCACAAACAGAGGGTTCACCTTTTTT  13805 GTGTAAACTTAAACTGTACATCCACAAACAGAGATAACGGTTCTCTTTTTTT  13805 GTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTT  13865 GTGTAAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAGAGCCGTT  13865 GTGTAAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTCGTCAGCAAAAAGAGCCGTT  13865 GTGTAAAACCTTAAACTGCATTTCACCAGTCCTTTTTCAGTTCTCGTCAGCAAAAAGAGCCGTTC  13865 GTGTAAAACCTTAAACTGCATTTCACCAGTCCTTTTTCAGCATAAAAAAAA	1102 ATATATGCCTTGAGCAACTGATAGCTGTCAACTGTCACTGTAATAGCTTC 116 14045 ATATATGCCTTGAGCAACTGATAGCTGCTGCTGCTGCTGTGACTGCTGCTGCTGCTGTGAGTGCTGCTGTGACTGTCACTTTTTGACATTGACGTGGCTGCTGACTGTCACTTTTTGCCCAA 122 14105 ATAGCACCTCTTTTTTTGACATACTTCGGGTAGTGCCGATCAACGTCTATTTTGCCCAA 122 1222 AAGTTGGCCCAGGCTTCCCGGTATCAACGGGAACTCAACTTTTTTTT	13425 IGAICTTCCGTCACAGATATTTATTCGGCGCAAGTGCGTCGGGTGATGCTGGTGTGTGT	14448
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QY         4800 TCAATTTGTTGCAACGAACGACACTATCAGTCAAAATAAAATCATTATTTGGGGCCCG         4859           Db         17010 TCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAATAAAATAAAT	RESULT 3 US-10-055-001A-24 Squarez 24, Application US/10055001A Publication No. US20030049835A1 Publication No. US20030049835A1 Publication No. US20030049835A1 APPLICANT: Waterhouse, Peter APPLICANT: Waterhouse, Peter APPLICANT: Helliwell, Christopher A. TITLE OF INVENTION: Using recombinational cloning TITLE OF INVENTION: Using recombinational cloning FILE REFERENCE: HELLGA CURRENT APPLICATION NUMBER: US/10/055,001A CURRENT PILING DATE: 2002-06-11 NUMBER OF SEQ ID NOS: 26 SOFTWARE: PatentIn version 3.1 SSOFTWARE: PatentIn version 3.1 SSOFTWARE: DNA CREANISM: Artificial sequence FEATURE: OTHER INFORMATION: acceptor vector pHELLSGATE8	10-055-001A-24	03   03   03   03   03   03   03   03	0y 442 ATTCATATACGCTAGTGCTGAAAATCATCTGCATCAAGAACAATTTCACAAC 501  Db 13385 ATTCATATACGCTAGTGCTCATAGATCCTGCAACATTTCAGAACAATTTCACAAC 13444  Qy 502 TCTTATACTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 561  Db 13445 TCTTATACTTTTCTTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA 561  Oy 562 CTAAACGTGATAAAGTTTCTGTACTTCTACTGCACTTGCATTTCAGCTCTATACTTA 13504  Oy 622 AGGGAGCTGAAAATTCTGTAAATTTCTACTATCGACCTGCAGACTGCTGTATA 621  Oy 622 AGGGAGCTGAAAATTTCTGTAATTTCTACTATCGACCTGCAGACTGCTGTATA 13564  Oy 622 AGGGAGCTGACATTTATATTCCCCAGAACATCAGGTTAATGGTGTATT 681

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                                                                                                                                                                                             DB 15;
                                                                                                                                                                                         Score 2563.2;
Pred. No. 0;
0; Mismatches
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   60363852
PRIOR APPLICATION NUMBER: US 6036;
PRIOR FILING DATE: 2003-03-14;
NUMBER OF SEQ ID NOS: 7
SCTUMARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 17476
TYPE: DNA
ORGANISM: Artificial
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Best Local Similarity 77.7%;
Matches 3651; Conservative
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Publication No. US20030175783A1
GENERAL INFORMATION:
APPLICANT: Waterhouse, Peter
APPLICANT: Wesley, Susan
APPLICANT: Helliwell, Chris
TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
FILE REFERENCE: COLINA-USE
CURRENT APPLICATION NUMBER: US/10/385,546
CURRENT FILING DATE: 2003-03-12
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14165 AAGTIGGCCCAGGGCTTCCCGGTATCAACAGGGACACCAGGATTTATTT		14448TCTCGAGGAATTCGGTACCCCAGCTAGGAATAATTTT 14492 1641 TCTTTTTCCTTTTAGTATAAATAGTTAAGTAAATAAGTAATTT 14492 14493 TCTTTTTCCTTTTAGTATAAAATAGTTAAGTGATGTAAATAGTATAATA	AATGTAAAAAATTGGCAAGTGATGTGTAAGAGGAAGAAGATAGT	1881 CAACTITCACCATAATGAAATAAGATCACTACCGGGGGGATTTTTTGAGTTATCGAGATT 1940 14726	2001 ATCCCAATGGCATCGTAAAGAACATTTGAGGCATTTCAGTCAG	2121 CAMGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATT 2180 14726
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1325 AGGANTGOTGOTNICOGGCCTACTGGTATTGOTGCACAATTAAATCAAATCAAA
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16553 CINTINGALIDATION ANTICOLOGICAL ANAMAGAGACHA CONCONCINCULTURE 15594  4465 TETRITICAL MACHINE AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND ANTICOLOGICAL AND

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US-10-055-001A-13/C

JUS-10-055-001A-13/C

SUBJUCTION NO. US20030049835A1

SUBJUCTION NO. US20030049835A1

SUBJUCANT: Wesley, Susan V.

APPLICANT: Wasley, Deter

APPLICANT: Wasley, Christopher A.

TITLE OF INVENTION: Wasing recombinational cloning

TITLE OF INVENTION: Using recombinational cloning

TITLE OF INVENTION: Using recombinational cloning

CURRENT APPLICATION UNMBER: US/10/055,001A

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.1

SEQ ID NO 13

LENGTH: 18691
    16605 TATGCAAAATCTAATTTAATATATTGATATTTATATATTATATATTTTACGTTTCTCGTTCAGCTT 16664
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OTHER INFORMATION: attP2 recombination site (complement)
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OTHER INFORMATION: chloramphenicol resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (10706)..(11324)
OTHER INFORMATION: right T-DNA border fragment
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LOCATION: (17890)..(17659)
OTHER INFORMATION: attP1 recombination site
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NAME/KEY: misc_feature
LOCATION: (13048)..(13279)
OTHER INFORMATION: attPl recombination site
FEATURE:
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OTHER INFORMATION: spectinomycin resistance
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OTHER INFORMATION: attP2 recombination site
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OTHER INFORMATION: ccdB selection marker
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OTHER INFORMATION: ccdB selection marker
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OTHER INFORMATION: pdk2 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial sequence
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LOCATION: (11674)..(13019)
OTHER INFORMATION: CAMV35S
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NAME/KEY: misc feature
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LOCATION: (15002)..(15
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NAME/KEY: misc_feature
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LOCATION: (7922)..(998)
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(165<u>5</u>1)..(16
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LOCATION:
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                                                            TCTTATACTTTCTCTTACAAGTCGTTCGGCTTCATCTGGATTTTCAGCCTCTATACTTA
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                    <u> AAGCCCTGGGCCAACTTTTGGCGAAAATGAGACGTTGATCGG</u>
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17184 CTGACGAGAACAGGG-----ACTGGTGAAATGCAGTTTAAGGTTTAACACCTATAAAAGA 17131
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                                                                           781 ACCACCGGGTAAAGTTCACGGGAGACTTTATCTGACAGCAGACGTGCACTGGCCAGGGGG
                                                                                                                                              841 ATCACCATCCGTCGCCCGGGCGTGTCATAATATCACTCTGTACATCCACAAACAGACGA
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                                                                                                          17130 GAGAGCCGTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTGACACGCCCGGGCGA
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       GAGACCGGCACACTGGCCATATCGGTGGTCATCATGCGCCAGCTTTCATCCCCCGATATGC
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                                                                                                                                                                                                                                                                                                                                                                           Score 1462.6; DB 15; Length 1869
Pred. No. 7.5e-233;
0; Mismatches 1889; Indels 104;
                                     synthase gene terminator region
                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
                                                                                                                                                                                                                                                               FEATURE:

NAME/KBY: misc feature

LOCATION: (2149)..(2706)

COLER INFORMATION: a left T-DNA border region
US-10-055-001A-13
                                                                                                          gene
                                                               NAME/KEY: misc feature
LOCATION: (264)...(496)
OTHER INFORMATION: nopaline synthase gene
FEATURE:
NAME/KEY: misc feature
LOCATION: (497)...(1442)
OTHER INFORMATION: nptlI coding region
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.1%;
Best Local Similarity 59.4%;
Matches 2920; Conservative
NAME/KEY: misc feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine
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                   CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOCTWARE: PATENTIN VERSION 3.1
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: plasmid pDONR201
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial sequence
FILE REFERENCE: 0942.5120001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (3495)..(4134)
; OTHER INFORMATION: Ori
US-10-151-690-21
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RMATION: attP2
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OTHER INFORMATION: Kmr
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LOCATION: (1099)..(1184)
OTHER INFORMATION: ccdA
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LOCATION: (656)..(961)
OTHER INFORMATION: ccdB
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LOCATION:
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Publication No. US20030124555A1
AEPLICANT: INFORMATION:
APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOU
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24.5%; Score 1193; DB 16;
Best Local Similarity 100.0%; Pred. No. 2.7e-188;
Matches 1193; Conservative 0; Mismatches C;
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OTHER INFORMATION: attPl recombination site
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LOCATION: (3794)..(4537)
OTHER INFORMATION: pUC oriV / RK2 oriT
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                                             TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: terminator
LOCATION: (73)..(100)
OTHER INFORMATION: 72
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OTHER INFORMATION: Cam(r)
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OTHER INFORMATION: Kan(r)
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OTHER INFORMATION: attP2
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                 LOCATION: (232)..(275)
OTHER INFORMATION: T1
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NAME/KEY: terminator
LOCATION: (232)..(275)
OTHER INFORMATION: T1
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(959)
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Publication No. US20030219902A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: House, Brent L
APPLICANT: Mortimer. Michael W
TITLE OF INVENTION: Methods and Vectors for Facilitating Site-Specific Recombination
FILE REFERENCE: WSUR-1-20291
CURRENT APPLICATION NUMBER: US/10/357,268
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/354,063
PRIOR FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
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Best Local Similarity 100.0%; Pred. No. 2.8e-188;
Matches 1193; Conservative 0; Mismatches 0;
                                                                                         ; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61
                                                               sequence
    version
                                                         ORGANISM: Artificial
SOFTWARE: Patentin
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Fublication No. US200301245581
GENERAL INPORMATION:
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: LI, XIAO
APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: BSROSITO, DOMINIC
APPLICANT: BSROSITO, DOMONIC
APPLICANT: BSROSITO, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 0942.512001
CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT APPLICATION NUMBER: US 10/1151,690
FRIOR APPLICATION NUMBER: US 10/151,690
PRIOR APPLICATION NUMBER: US 60/291,973
FRIOR PRILING DATE: 2002-05-21
FRIOR APPLICATION NUMBER: US 60/291,973
FRIOR FILING DATE: 2001-05-21
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0.0.1   TAACGGCTCTCTTTTATAGGTGTAAACCTTAAACTGCATTTCACCAGTCCCTGTTCTC   0.0   0.0   1   1   1   1   1   1   1   1   1	Qy         1081         CAGACCGGAGATATTGACATCATATATGCCTTGAGCAACTGATAGCTGTCGCTGTCAACT         1140           Db         4484         CAGACCGGAGATATTGACATATATATGCCTTGAGCAACTGATGCTGTCAACT         4425           Qy         1141         GTCACTGTAATAGGCTGCTTCATAGGCACCTCTTTTTGACATACTTCGGGTA         1193           Db         4424         GTCACTGTAATAGGCTGCTTCATAGCACACCTCTTTTTGACATACTTCGGGTA         4372	ULT 11 10-15-690-62 ublication US/10151690 ublication OS US2030124555A1 APPLICANT: BRASCH, MICHAEL A. APPLICANT: BRASCH, MICHAEL A. APPLICANT: BRASCH, MICHAEL A. APPLICANT: BRASCH, MICHAEL A. APPLICANT: BRASCH, MICHAEL A. APPLICANT: BYED. DOWING APPLICANT: LI, XIADO DOMINIC APPLICANT: BYED. DOWINIC APPLICANT: DAYDON R.N. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCCURRENT FILING DATE: 2002-05-21 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION NUMBER: US 60/291,973 PRIOR APPLICATION N	Db : 918 TGAGCAATGCTTTTTTATAATGCCAACTTTGTAAAAAAGCTGATATCGAAAAGCTGATATCGAAAAA

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RESULT 13

US-10-151-690-64

i Sequence 64, Application US/10151690

i Publication No. US20030124555A1

GENERAL INFORMATION:
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID

APPLICANT: ELSPOSITO, DOMINIC
APPLICANT: BXRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO

CURRENT APPLICATION NUMBER: US/10/151,690

PRIOR PEPLICATION NUMBER: US 60/291,973

PRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin Version 3.1

TENTIFY OF SECTION NUMBER: US 60/291,973

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin Version 3.1
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Pred. No. 3e-187;
0; Mismatches 4; Indels 0;
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OTHER INFORMATION: plasmid pDONR212
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Best Local Similarity 99.7%;
Matches 1189; Conservative
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Pred. No. 3e-187;
0; Mismatches
CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR PILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63
                                                                                                                                                                                                                                                                                                                     24.4%;
99.7%;
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity
Matches 1189; Conserv
                                                                                                                                                         SEQ ID NO 63
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                                         USE
APPLICANT: Wanner, Barry
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF 1;
FILE REPERENCE: 290.00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/328,642
PRIOR APPLICATION NUMBER: 60/375,059
PRIOR APPLICATION NUMBER: 60/375,059
PRIOR PILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 4782
                                         OF
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                                                                                                                                                                                                                                                                                                                                                    Score 876.4; DB 13;
Pred. No. 1.1e-135;
0; Mismatches 441;
                                                                                                                                                                                                                                                                                               OTHER INFORMATION: CRIM plasmid
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Best Local Similarity 71.6%;
Matches 1259; Conservative (
                                                                                                                                                                                                                                                             ORGANISM: artificial FEATURE:
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 ATGCCGTATTAAATCATAAAAGAAATAAGAAAAAAGAGGTGCGAGCCTCTTTTTGTGTG
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                                                    CCTTCCAAATGTTCTTCTCAAACGGAATCGTCGTATCCAGCCTACTCGCTATTGTCCTCA
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4060

2031 4120 2091 4000 2211 3940 2271 3880 2331 3820 2391 3700 2511 3640 2571 3580

2572 ATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATCGCGTGGA 2631

3639 CIGALGCCGCTGGCGATICAGGITCATCATGCCGICTGTGATGGCTTCCATGTCGGCAGA

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Sequence 20, Application US/10270176 Publication No. US20040033608A1 GENERAL INFORMATION:

RESULT 14 US-10-270-176-20/c

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2512 CTGATGCCGCTGGCGATTCAGGTTCATGTCGTCTGTGATGGCTTCCATGTCGGCAGA

3760 2451

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S-10-270-176-19/c
Sequence 19, Application US/10270176
Publication No. US20040033608A1
GENERAL INPORMATION:
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ilarity 71.6%;
Conservative
                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: CRIM
US-10-270-176-19
                                                                                                                                                                                                                            TYPE: DNA ORGANISM: artificial
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Matches 1259; Conserv
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                                                                -TTTTTTAAGGCAGTTATTGGTGCCTCACT
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                                     TCCGGCTTACTAAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTATA
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APPLICANT: Haldimann, Andreas

TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF 1

TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF 1

CURRENT APPLICATION NUMBER: US/10/270,176

CURRENT FILING DATE: 2002-10-10

PRIOR APPLICATION NUMBER: 60/328,642

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2002-04-24

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Patentin version 3.0

SEQ ID NO 19

LENGTH: 6742
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 782)
Raul, S., Town, C.D., Bowman, C.L., Van Aken, S.E., Utterback, T.V.,
Feldblyum, T.V. and Fraser, C.M.
Survey sequencing of Arabidopsis thaliana BAC T20G10
Unpublished (2001)
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Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
From Wash. U contig 1370. Caution: the DNA in this BAC may be from Seme non-Arabidopsis source
Seq primer: TF
                                                                                  BZ070235
BZ069987
                                                                                                          BZ070648
BH960653
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BH936398
BZ085715
BH920449
BZ063552
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BZ085150
BZ084529
BZ083912
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BZ042047
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BZ069550
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BZ076353
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BH242215
BH242215.1 GI:16917233
GSS.
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BH242215/c
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  BH242215 ATZFD43TF
CC219264 CH261-114
BZ069663 ljt36e08.
BZ071317 lju13g05.
                                                                               8, 2004, 10:39:35; Search time 7540.15 Seconds (without alignments) 19251.609 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                 27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                               US-10-055-001B-13_COPY_13040_17900
4861
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CC219264
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BZ071317
                                                            using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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Maximum DB seq length: 2000000000
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Score

Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female"
/cell line="UCD001, inbred 256"
/clone lib="CH261"
/note="Vector: pTARBAC2.1; Site 1: EcoR1; Site 2: EcoR1;
CH261 Female Chicken library - For library and clone ordering information: http://www.chori.org/bacpac"
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (Sassa 1 to 939)

Kremitzki, C., Higginbotham, J., Mylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

Gallus gallus BAC End Reads

Unpublished (2003)

Contact: Richard K. Milson
CH261-114B11_Sp6.1 CH261 Gallus gallus genomic clone CH261-114B11,
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                                                                                                                                                                                                                                                                                                              Genome Sequencing Center
Washington University School of Medicine
Email: submissioneswateon.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 36
High quality sequence stop: 800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .939
/organism="Gallus gallus"
/moi_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-114B11"
          genomic survey sequence.
CC219264
                                                          CC219264.1 GI:30541330 GSS.
                                                                                                 Gallus gallus (chicken)
Gallus gallus
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/organism="Arabidopsis thaliana"

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia"

/db_xref="taxon:3702"

/clone="ATZF"

/clone lib="ATZF"

/clone lib="ATZF"

/note="Vector: PHOS2; Site_1: BstXI; 2-3 kb she

DNA inserted into PHOS2 using BstXI linkers"
                                                                                                                                                                                                                                                                                                      2;
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Pred. No. 8.6e-122;
0; Mismatches 10; Indels
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Db 498 ACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACC 439  Qy 2354 TGGCCTATTTCCCTAAAGGGTTTATTGAAAATTTTCGTCTCAGCCAATCCCTGGG 2413  Db 438 TGGCCTATTTCCCTAAAGGGTTTATTGAAATTTTTTTTTCGTCTCAGCCAATCCCTGGG 379  Qy 2414 TGAGTTTCACCAGTTTTGATTTAAAACGTGGCCAATTTGACCTCTCGCCCCGTTT 2473  Db 378 TGAGTTTCACCAGTTTTGATTTAAAACGTGGCCAATTTGACCACTTCTCGCCCCCGTTT 319  Qy 2474 TCACCATGGGCAAATATTATACGCAGCGACAAGGTGCTGAAGCTGCCGCTGGCGATTCAGG 259  Db 318 TCACCATGGGCAAATATTATACGCAGCGGACAAGGTGCTGATGCCGCTGGCGATTCAGG 259  Qy 2534 TTCATCATGCCGTTGTGATGGCTTCCATGTCGGCCAGATTACAACGT 2593  Qy 2534 TCATCATGCGATGATGATGATGATGAAATACAAAGTTTAATGAATTACAACAGT 199  Qy 2594 ACTGCGATGACGCGGCGGCAAAT 2623  Db 198 ACTGCGATGACGCGGCGCGTAAT 2623	SULT 3  G09663/C  CUS  EXC69663  FINITION   1j13608.D1 B.oleracea002 Brassic sequence.  CESSION BZ069663.1 GI:23685962  WORDS  WORDS  GSS.  URCE  Brassica oleracea  GRANISM Brassica oleracea  CRANISM Brassica oleracea  Eukaryota, Viridiplantae, Streptc Spermatophyta; eucrosids II; Brassicales, rosids, eucosids II; Brassicales, rosids, eucosids II; Brassicales, NagnHORS  FERENCE  Cosids, eucosids II; Brassicales, Nash, W., Rabinovicz, P.D. and Will Whole genome shotgun reads from FOURTILE  Whole genome shotgun reads from FOURTILE  Whole genome Sequencing Center  Washington University School of Nashington University School of Namani Branis gubmissions@watcon.wastl.  Flate: 11436 row: e column: 98	Seq primer: -21UFpOT forward Class: Shotgun High quality sequence start: 8 High quality sequence stop: 551.  FEATURES  Location/Qualifiers  1. 783 / organism="Brassica oleracea" / mol_type="genomic DNA" / db xref="taxon:3712" / clone_lib="B.oleracea002" / flowering buds: DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shorgun library prepared at Washington University Genome Sequencing Center."  Query Match  Query Match  14.3%; Score 697.4; DB 28; Length 783; Best Local Similarity 97.8%; Pred. No. 1.5e-115; Matches 707; Conservative 0; Mismatches 16; Indels 0; Gaps 0;	Db 752 ACTIVICALCATAAGCTITAATGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAA 693

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2263 ACGITITCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATAT 2322
                                                                        848 bp DNA linear GSS 10-OCT-2002
B.oleracea002 Brassica oleracea genomic, genomic survey
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Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                                                                                                                                                                      Brassica oleracea
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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larity 97.8%; Pred. No. 1.4e-115;
Conservative 0; Mismatches 16; 1
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/db_xref="taxon:3712"
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Location/Qualifiers
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Genome Sequencing Center
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.larity 97.8%; Pred. No. 1.4e-115;
Conservative 0; Mismatches 16; ]
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
Class: shotgun
High quality sequence start: 8
High quality sequence stop: 551.
Location/Qualifiers
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Brassica oleracea
Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II, Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 789)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
            CAGGAGCTAAGGAAGCTAAAATGGAGAAAAA 1973
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                                                                                                                 AATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGC
                                                                                                                                                                  ATTICAGICAGITGCICAAIGIACCIAIAACCAGACCGIICAGCIGGAIAITACGGCCII
                                                                                         AATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGC
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
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1 (bases 1 to 903)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.

Burns, J.L., Kaul, R. and olsen, M.V.

Facomones Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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                                                                                                                                      AATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTG
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                                                                                             384 TCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAAGGTTTATTGAG
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/clone="pacs2-164 8345"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
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Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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/organism="Pseudomonas at /mol_type="genomic DNA"
/strain="2-164"
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Location/Qualifiers
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Email: craymond@
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/db xref="taxon:3712"

/db xref="taxon:3712"

/clone lib="B.oleracea002"

/note="Weetor: pOTW-13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TolloODH3 buds provided by Propusal Soborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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| Contact: Richard K. Wilson Genome Sequencing Center Washington University School of Medicine Email: submissions@wastson.wustl.edu
| Flate: Iki38 row: a column: 06 |
| Plate: Iki38 row: a column: 06 |
| Class: shotgun |
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Pred. No. 2.2e-115;
----rhes 17;
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/db xref="taxon:3712"
/clone lib="B.oleracea002"
/clone lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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Pred. No. 1.6e-115;
0; Mismatches 19;
                                                                                                                                                                           /organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
  Seg primer: -21UPpO1 LOLTCO
Class: shotgun
High quality sequence start: 20
High quality sequence stop: 551.
Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
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Washington University School of Medicine
Brail: submissions@watson.wustl.edu
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
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Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location/Qualifiers
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                                                                                     GI:23701053
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                                                                                           Corganism="Brassica oleracea"

[mol Lype="genomic DNA"]

[db Aref="taxon:3712"]

[clone lib="B.oleracea002"]

[note="vector: pOTw13; Whole genome shotgun library from fnote="vector: pOTw13; Whole genome shotgun library from prep using Brassica oleracea TO100DH3 buds provided by prep using Brassica oleracea TO100DH3 buds provided by howas provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
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llarity 99.6%; Pred. No. 3.7e-115;
Conservative 0; Mismatches 3;
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High quality sequence stop: 551.
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/organia="Brassica oleracea"
/organia="Brassica oleracea"
/db_xref="taxon:3712"
/db_xref="taxon:3712"
/clone lib="Booleracea002"
/note="Vector: poTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea Tolo00DH3 buds provided by Thosmas Obborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
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Bukaryota, Viridiplantae, Eudicotyledons; core eudicots;
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1 (bases 1 to 785)
Delehanury, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nab, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
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lkj38a04.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
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                S Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nabhow, K., Rabinowicz, P.D. and Wilson, R.K.
Nabh, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: 114/38 row: a column: 04
Seq primer: -21Uppor forward
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location (Qualifiers)
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Bukaryota, Viridiplantae; Streptophyta; Euchorosics;
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rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 797)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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Mashington University School of Medicine
Email: submissions@wateon.wustl.edu
Plate: lkf31 row: c column: 12
Seq primer: -28RPpOT reverse
Class: shotgun
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/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
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Conservative 0; Mismatches 18;
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B.oleracea002 Brassica oleracea genomic, genomic survey
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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Pred. No. 6.4e-115;
0; Mismatches 7;
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Genome Sequencing Center
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Inote="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using buds. DNA was purified from a provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the Shotgun library prepared at Washington University Genome Sequencing Center."
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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rosids, eurosids II, Brassicales, Brassicaceae, Brassica.

1 (bases 1 to 725)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,
Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shorgun reads from Brassica oleracea
Unpublished (2002)
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
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db_xref="taxon:3712"
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Class: shotgun
High quality sequence start: 22
High quality sequence stop: 551.
Location/Qualifiers
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